

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:30:00 ; Search time 39 Seconds
(without alignments)
695.758 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDEREQMAISGGFIRRTNA.....SNKTRIDEANQRATKMLGSG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	57.0	124	13	Q93578
2	49	57.0	143	6	Q9GM34
3	32	37.2	206	13	Q8AXM2
4	32	37.2	206	13	Q8AXM1
5	22	25.6	203	13	Q93579
6	10	11.6	210	11	O35620
7	10	11.6	210	11	O70377
8	10	11.6	210	11	O09044
9	10	11.6	221	11	Q9D3L3
10	9	10.5	204	13	Q8JIS7
11	9	10.5	214	13	Q7ZVE4
12	8	9.3	90	5	O96578
13	8	9.3	125	5	O96576
14	8	9.3	156	16	Q892G6
15	8	9.3	158	5	O96575
16	8	9.3	195	5	O96574

17	8	9.3	357	16	Q99W76
18	8	9.3	593	16	O24909
19	8	9.3	1135	5	Q9NJQ4
20	7	8.1	74	10	Q93VW1
21	7	8.1	83	2	O85432
22	7	8.1	83	2	O85440
23	7	8.1	83	2	O85439
24	7	8.1	83	2	O85431
25	7	8.1	162	16	Q8DF43
26	7	8.1	170	10	Q9SBC2
27	7	8.1	171	10	Q9ZSW8
28	7	8.1	197	2	P95796
29	7	8.1	212	5	O44419
30	7	8.1	212	5	O76338
31	7	8.1	226	11	Q9CVN5
32	7	8.1	228	4	Q8NA63
33	7	8.1	271	4	Q8N6Q1
34	7	8.1	285	16	Q926K3
35	7	8.1	303	11	Q9D9D5
36	7	8.1	350	16	Q97EN6
37	7	8.1	380	16	Q8X9Q9
38	7	8.1	384	16	Q836N1
39	7	8.1	387	16	Q9CJ77
40	7	8.1	393	2	Q8GR72
41	7	8.1	396	16	Q8U6M7
42	7	8.1	407	16	Q7TV99
43	7	8.1	414	5	Q93231
44	7	8.1	473	10	Q8S0Z9
45	7	8.1	562	13	Q7SZP4

ALIGNMENTS

RESULT 1

Q93578 ID Q93578 PRELIMINARY; PRT; 124 AA.
AC Q93578;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN SNAP25A OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99057281; PubMed=9843147;
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammer D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage."
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091593; AAC64289.1; -.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
FT NON TER 1
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 57.0%; Score 49; DB 13; Length 124;
Best Local Similarity 100.0%; Pred. No. 5.3e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSKNTRIDEANQRATKMLGSG 86

Db	76	GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG	124
RESULT 2			
Q9GM34			
ID	Q9GM34	PRELIMINARY;	PRT; 143 AA.
AC	Q9GM34;		
DT	01-MAR-2001 (TReMBLrel. 16, Created)		
DT	01-MAR-2001 (TReMBLrel. 16, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;		
OC	Cercopithecinæ; Macaca.		
OX	NCBI_TaxID=9541;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,		
RA	Suzuki Y., Sugano S., Hashimoto K.;		
RT	"Isolation of full-length cDNA clones from macaque brain cDNA		
RT	libraries.";		
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB049852; BAB16738.1; -.		
DR	InterPro; IPR000928; SNAP-25.		
DR	InterPro; IPR000727; T_SNARE.		
DR	Pfam; PF00835; SNAP-25; 1.		
DR	Pfam; PF05739; SNARE; 1.		
DR	SMART; SM00397; t_SNARE; 1.		
DR	PROSITE; PS50192; T_SNARE; 1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;		
Query Match	57.0%;	Score 49;	DB 6; Length 143;
Best Local Similarity	100.0%;	Pred. No. 6e-44;	
Matches	49;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	38	GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG	86
Db	95	GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG	143
RESULT 3			
Q8AXM2			
ID	Q8AXM2	PRELIMINARY;	PRT; 206 AA.
AC	Q8AXM2;		
DT	01-MAR-2003 (TReMBLrel. 23, Created)		
DT	01-MAR-2003 (TReMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	SNAP25a.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF335586; AAO13788.1; -.		
DR	InterPro; IPR000928; SNAP-25.		
DR	InterPro; IPR000727; T_SNARE.		
DR	Pfam; PF00835; SNAP-25; 1.		
DR	Pfam; PF05739; SNARE; 1.		
DR	SMART; SM00397; t_SNARE; 2.		
DR	PROSITE; PS50192; T_SNARE; 2.		
SQ	SEQUENCE 206 AA; 23122 MW; 2D1D0FD3550C1DDF CRC64;		
Query Match	37.2%;	Score 32;	DB 13; Length 206;
Best Local Similarity	100.0%;	Pred. No. 9.8e-26;	
Matches	32;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	38	GNLRHMDMGNEIDTQNRQIDRIMEKADSNK	69
Db	158	GNLRHMDMGNEIDTQNRQIDRIMEKADSNK	189
RESULT 4			
Q8AXM1			
ID	Q8AXM1	PRELIMINARY;	PRT; 206 AA.
AC	Q8AXM1;		
DT	01-MAR-2003 (TReMBLrel. 23, Created)		
DT	01-MAR-2003 (TReMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	SNAP25b (Hypothetical protein).		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB049852; BAB16738.1; -.		
DR	InterPro; IPR000928; SNAP-25.		
DR	InterPro; IPR000727; T_SNARE.		
DR	Pfam; PF00835; SNAP-25; 1.		
DR	Pfam; PF05739; SNARE; 1.		
DR	SMART; SM00397; t_SNARE; 1.		
DR	PROSITE; PS50192; T_SNARE; 1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;		
Query Match	57.0%;	Score 49;	DB 6; Length 143;
Best Local Similarity	100.0%;	Pred. No. 6e-44;	
Matches	49;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	38	GNLRHMDMGNEIDTQNRQIDRIMEKADSNK	69
Db	158	GNLRHMDMGNEIDTQNRQIDRIMEKADSNK	189
RESULT 4			
Q8AXM1			
ID	Q8AXM1	PRELIMINARY;	PRT; 206 AA.
AC	Q8AXM1;		
DT	01-MAR-2003 (TReMBLrel. 23, Created)		
DT	01-MAR-2003 (TReMBLrel. 23, Last sequence update)		
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)		
DE	SNAP25b (Hypothetical protein).		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;		
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB049852; BAB16738.1; -.		
DR	InterPro; IPR000928; SNAP-25.		
DR	InterPro; IPR000727; T_SNARE.		
DR	Pfam; PF00835; SNAP-25; 1.		
DR	Pfam; PF05739; SNARE; 1.		
DR	SMART; SM00397; t_SNARE; 1.		
DR	PROSITE; PS50192; T_SNARE; 1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;		
Query Match	37.2%;	Score 32;	DB 13; Length 206;

Best Local Similarity 100.0%; Pred. No. 9.8e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWMALDGMGNEIDTQNRQIDRIMEKADSNK 69
Db 158 GNLRHWMALDGMGNEIDTQNRQIDRIMEKADSNK 189

RESULT 5
O93579
ID O93579 PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein
DE 25.2).
GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage."
RL J. Neurosci. Res. 0:0-0(1998).
DR EMBL; AF091594; AAC64290.1; -.
DR EMBL; AF091596; AAC73007.1; -.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DDDC93F38 CRC64;

Query Match 25.6%; Score 22; DB 13; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 ADSNKTTRIDEANORATKMLGSG 86
Db 182 ADSNKTTRIDEANORATKMLGSG 203

RESULT 6
O35620
ID O35620 PRELIMINARY; PRT; 210 AA.
AC O35620;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 23kDa synaptosomal associated protein.
GN SNAP23 OR MSNAP-23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Olken S.K., Doerre S., Corley R.B.;
RT "SNARE expression in mouse plasma cells."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF007169; AAB62932.1; -.
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
SQ SEQUENCE 210 AA; 23277 MW; FB752FB58D5AE6D9 CRC64;

Query Match 11.6%; Score 10; DB 11; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MALDMGNEID 52
Db 168 MALDMGNEID 177

RESULT 7
O70377
ID O70377 PRELIMINARY; PRT; 210 AA.
AC O70377;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNAP-23.
GN SNAP-23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162237; PubMed=10051443;
RA St-Denis J.F., Cabaniols J.P., Cushman S.W., Roche P.A.;
RT "SNAP-23 participates in SNARE complex assembly in rat adipose
RT cells."
RL Biochem. J. 338:709-715(1999).
DR EMBL; AF052596; AAC06031.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T_SNARE; 2.
SQ SEQUENCE 210 AA; 23235 MW; 0D63E3A6F9FE3BA2 CRC64;

Query Match 11.6%; Score 10; DB 11; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MALDMGNEID 52
Db 168 MALDMGNEID 177

RESULT 8
O09044
ID O09044 PRELIMINARY; PRT; 210 AA.
AC O09044;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SYNDET (SNAP-23) (Synaptosomal-associated protein, 23KD).
GN SNAP23 OR SNDET.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat;
RX MEDLINE=97312558; PubMed=9168999;
RA Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H.,
RA Niki T., Okazawa H., Kubota T., Kasuga M.;
RT "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.";

RL Biochem. Biophys. Res. Commun. 234:257-262(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97220227; PubMed=9067602;
 RA Wang G., Witkin J.W., Hao G., Bankaitis V.A., Scherer P.E.,
 RA Baldini G.;
 RT "Syndet is a novel SNAP-25 related protein expressed in many
 RT tissues";
 RL J. Cell Sci. 110:505-513(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Vaidyanathan V.V., Roche P.A.;
 RT "Structure and chromosomal localization of the mouse SNAP-23 gene";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL; AB000822; BAA20345.1; -;
 DR EMBL; U73143; AAB53597.1; -;
 DR EMBL; AF213257; AAF23503.1; -;
 DR EMBL; AF213251; AAF23503.1; JOINED.
 DR EMBL; AF213252; AAF23503.1; JOINED.
 DR EMBL; AF213253; AAF23503.1; JOINED.
 DR EMBL; AF213254; AAF23503.1; JOINED.
 DR EMBL; AF213255; AAF23503.1; JOINED.
 DR EMBL; AF213256; AAF23503.1; JOINED.
 DR EMBL; AK019162; BAB31577.1; -;
 DR PIR; JC5512; JC5512.
 DR MGD; MGI:109356; Snap23.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t SNARE; 2.
 DR PROSITE; PS50192; t SNARE; 2.
 SQ SEQUENCE 210 AA; 23261 MW; 6919E127E16BA2C9 CRC64;
 Query Match 11.6%; Score 10; DB 11; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 MALDMGNEID 52
 Db 168 MALDMGNEID 177
 RESULT 9
 Q9D3L3 PRELIMINARY; PRT; 221 AA.
 ID Q9D3L3
 AC Q9D3L3
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Synaptosomal-associated protein, 23kD.
 GN SNAP23.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL; AK017311; BAB30686.1; -;
 DR MGD; MGI:109356; Snap23.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t SNARE; 2.
 DR PROSITE; PS50192; t SNARE; 2.
 SQ SEQUENCE 221 AA; 24550 MW; 368862BE7232DEFB CRC64;
 Query Match 11.6%; Score 10; DB 11; Length 221;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 MALDMGNEID 52
 Db 179 MALDMGNEID 188
 RESULT 10
 Q8JIS7 PRELIMINARY; PRT; 204 AA.
 ID Q8JIS7
 AC Q8JIS7
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SNAP-23.
 GN XOSNAP-23.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 ON NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mashima J., Nagahama M., Hatzuzawa K., Tani K., Kikuchi F.,
 RA Horigome T., Yamamoto A., Tagaya M.;
 RT "Evidence for the involvement of alpha-SNAP and SNAP-23 in the fusion
 RT of nuclear membrane vesicles";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033718; BAC06591.1; -;

DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 2.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS50192; T SNARE; 1.
SQ SEQUENCE 204 AA; 22771 MW; D034F75E638E8805 CRC64;
Query Match 10.5%; Score 9; DB 13; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 68 NKTRIDEAN 76
Db 188 NKTRIDEAN 196
RESULT 11
Q7ZVE4
ID Q7ZVE4 PRELIMINARY; PRT; 214 AA.
AC Q7ZVE4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to synaptosomal-associated protein, 23 kDa.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045896; AAH45896.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS50192; T SNARE; 2.
SQ SEQUENCE 214 AA; 23670 MW; 5B43808BA6645A4C CRC64;
Query Match 10.5%; Score 9; DB 13; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44 ALDMGNEID 52
Db 175 ALDMGNEID 183
RESULT 12
O96578
ID O96578 PRELIMINARY; PRT; 90 AA.
AC O96578;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-5 (Fragment).
GN SNAP-5.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberridae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
PL

DR EMBL; AF091602; AAC69878.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 1.
DR PROSITE; PS50192; T SNARE; 1.
FT NON TER 1
SQ SEQUENCE 90 AA; 10136 MW; E502D8954676B9F7 CRC64;
Query Match 9.3%; Score 8; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRI 61
Db 60 QNRQIDRI 67
RESULT 13
O96576
ID O96576 PRELIMINARY; PRT; 125 AA.
AC O96576;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-3 (Fragment).
GN SNAP-3.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberridae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
DR EMBL; AF091600; AAC69876.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 1.
DR PROSITE; PS50192; T SNARE; 1.
FT NON TER 1
SQ SEQUENCE 125 AA; 13985 MW; 72B032879858C316 CRC64;
Query Match 9.3%; Score 8; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRI 61
Db 94 QNRQIDRI 101
RESULT 14
Q892G6
ID Q892G6 PRELIMINARY; PRT; 156 AA.
AC Q892G6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phage-related protein.
GN CTC02133.
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / E88;
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baumer S., Fricke W.F., Wierzer A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL; AE015943; AAC36629.1; --
KW Complete proteome.
SQ SEQUENCE 156 AA; 17919 MW; FC226BEAD767CE55 CRC64;

Query Match 9.3%; Score 8; DB 16; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 VSGILGNL 40
Db 63 VSGILGNL 70

RESULT 15
O96575 PRELIMINARY; PRT; 158 AA.
AC O96575;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-2 (Fragment).
GN SNAP-2.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence
RT variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
DR EMBL; AF091599; AAC69875.1; --
FT NON TER 1
SQ SEQUENCE 158 AA; 17926 MW; 6AEE26EBA70D0358 CRC64;

Query Match 9.3%; Score 8; DB 5; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRI 61
Db 109 QNRQIDRI 116

RESULT 16
O96574 PRELIMINARY; PRT; 195 AA.
AC O96574;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-1.
GN SNAP-1.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence
RT variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
DR EMBL; AF091598; AAC69874.1; --
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS0192; T SNARE; 2.
SQ SEQUENCE 195 AA; 21759 MW; 7DB7C1790EC84151 CRC64;

Query Match 9.3%; Score 8; DB 5; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRI 61
Db 182 QNRQIDRI 189

RESULT 17
Q99W76 PRELIMINARY; PRT; 357 AA.
ID Q99W76
AC Q99W76;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SAV0527 (Hypothetical protein MW0482).
GN SAV0527 OR SA0485 OR MW0482.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP003359; BAB56689.1; --
DR EMBL; AP003130; BAB41715.1; --
DR EMBL; AP004823; BAB94347.1; --
DR PIR; H89819; H89819.
DR InterPro; IPR002716; PIN.
DR InterPro; IPR006596; PINC.
DR InterPro; IPR002792; TRAM.

```
DR Pfam; PF01850; PIN; 1.
DR Pfam; PF01938; TRAM; 1.
DR SMART; SM00670; PIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 357 AA; 39586 MW; 7F81D25CF53CC6C9 CRC64;

Query Match          9.3%; Score 8; DB 16; Length 357;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FRRVTNA 20
Db 60 FRRVTNA 67

RESULT 18
O24909          PRELIMINARY; PRT; 593 AA.
AC O24909;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP0080.
GN HP0080.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AB000529; AAD07151.1; -.
DR PIR; H64529; H64529.
DR TIGR; HP0080; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 593 AA; 65970 MW; 731C02B2EB7C815A CRC64;

Query Match          9.3%; Score 8; DB 16; Length 593;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNLR 41
Db 81 SGILGNLR 88

RESULT 19
Q9NJQ4          PRELIMINARY; PRT; 1135 AA.
AC Q9NJQ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SEC7-related protein.
GN SEC7.
OS Parametium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Parametium.
OX NCBI_TaxID=5888;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=29S;
RA Nair S., Guerra C.F., Satir P.;
RT "A SEC7-related protein in Parametium."
RL FASEB J. 0-0-0(1999).
DR EMBL; AF129515; AAF36486.1; -.
DR HSSP; Q99418; 1PBV.
DR InterPro; IPR000904; Sec7.
DR Pfam; PF01369; Sec7; 1.
DR SMART; SM00222; Sec7; 1.
DR PROSITE; PS50190; SEC7; 1.
SQ SEQUENCE 1135 AA; 132880 MW; A95B0EC5C90A9BDB CRC64;

Query Match          9.3%; Score 8; DB 5; Length 1135;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIMEX 64
Db 675 QIDRIMEX 682

RESULT 20
Q93VW1          PRELIMINARY; PRT; 74 AA.
AC Q93VW1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0560B06.24 protein (P0043B10.16 protein).
GN P0560B06.24 OR P0043B10.16.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0560B06."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0043B10."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003281; BAB64757.1; -.
DR EMBL; AP003236; BAB64727.1; -.
DR Gramene; Q93VW1; -.
SQ SEQUENCE 74 AA; 8288 MW; 8218A251C59901E5 CRC64;

Query Match          8.1%; Score 7; DB 10; Length 74;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 MGNEIDT 53
Db 1 MGNEIDT 7

RESULT 21
O85432          PRELIMINARY; PRT; 83 AA.
AC O85432;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major outer membrane lipoprotein I (Fragment).
GN OPRI.
```

OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LMG 5939;

RX MEDLINE=89313294; PubMed=2473376;

RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,

RA Hannaert V., Hubert J.C.;

RT "Cloning and analysis of the gene for the major outer membrane

RT lipoprotein from Pseudomonas aeruginosa.";

RL Mol. Microbiol. 3:421-428(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LMG 5939;

RX MEDLINE=99069329;

RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,

RA Cornelis P.;

RT "Sequence diversity of the oprI gene, coding for major outer membrane

RT lipoprotein I, among rRNA group I pseudomonads.";

RL J. Bacteriol. 180:6551-6556(1998).

DR EMBL; AF065971; AAD03526.1; -.

DR InterPro; IPR000437; Prok_lipoprot S.

DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

KW Lipoprotein.

FT NON TER 83

SQ SEQUENCE 83 AA; 8683 MW; DD5E436ED924DBA9 CRC64;

Query Match

Best Local Similarity 8.1%; Score 7; DB 2; Length 83;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 DEANORA 79

Db 67 DEANORA 73

RESULT 22

O85440

ID O85440 PRELIMINARY; PRT; 83 AA.

AC O85440;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Major outer membrane lipoprotein I (Fragment).

GN OPRI.

OS Pseudomonas tolaasii.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=29442;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LMG 2342;

RX MEDLINE=89313294; PubMed=2473376;

RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,

RA Hannaert V., Hubert J.C.;

RT "Cloning and analysis of the gene for the major outer membrane

RT lipoprotein from Pseudomonas aeruginosa.";

RL Mol. Microbiol. 3:421-428(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LMG 2342;

RX MEDLINE=99069329;

RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,

RA Cornelis P.;

RT "Sequence diversity of the oprI gene, coding for major outer membrane

RT lipoprotein I, among rRNA group I pseudomonads.";

RL J. Bacteriol. 180:6551-6556(1998).

DR EMBL; AF065979; AAD03534.1; -.

DR InterPro; IPR000437; Prok_lipoprot S.

DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

KW Lipoprotein.

FT NON TER 83
 SQ SEQUENCE 83 AA; 8826 MW; FB5F436ED924DBBA CRC64;

Query Match 8.1%; Score 7; DB 2; Length 83;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 DEANORA 79

Db 67 DEANORA 73

RESULT 23

O85439

ID O85439 PRELIMINARY; PRT; 83 AA.

AC O85439;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Major outer membrane lipoprotein I (Fragment).

GN OPRI.

OS Pseudomonas fluorescens.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=294;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LMG 5833;

RX MEDLINE=89313294; PubMed=2473376;

RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,

RA Hannaert V., Hubert J.C.;

RT "Cloning and analysis of the gene for the major outer membrane

RT lipoprotein from Pseudomonas aeruginosa.";

RL Mol. Microbiol. 3:421-428(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LMG 5833;

RX MEDLINE=99069329;

RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,

RA Cornelis P.;

RT "Sequence diversity of the oprI gene, coding for major outer membrane

RT lipoprotein I, among rRNA group I pseudomonads.";

RL J. Bacteriol. 180:6551-6556(1998).

DR EMBL; AF065978; AAD03533.1; -.

DR InterPro; IPR000437; Prok_lipoprot S.

DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

KW Lipoprotein.

FT NON TER 83

SQ SEQUENCE 83 AA; 8826 MW; FB5F436ED924DBBA CRC64;

Query Match

Best Local Similarity 8.1%; Score 7; DB 2; Length 83;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 DEANORA 79

Db 67 DEANORA 73

RESULT 24

O85431

ID O85431 PRELIMINARY; PRT; 83 AA.

AC O85431;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Major outer membrane lipoprotein I (Fragment).

GN OPRI.

OS Pseudomonas corrugata.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=47879;

RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 2172;
 RX MEDLINE=89313294; PubMed=2473376;
 RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,
 RA Hannaert V., Hubert J.C.;
 RT "Cloning and analysis of the gene for the major outer membrane
 RT lipoprotein from *Pseudomonas aeruginosa*.";
 RL Mol. Microbiol. 3:421-428(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 2172;
 RX MEDLINE=99069329;
 RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,
 RA Cornelis P.;
 RT "Sequence diversity of the oprI gene, coding for major outer membrane
 RT lipoprotein I, among rRNA group I pseudomonads.";
 RL J. Bacteriol. 180:6551-6556(1998).
 DR EMBL; AF065970; AAD03525.1; -;
 DR InterPro; IPR000437; Prok lipoprot S.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Lipoprotein.
 FT NON_TER 83 83
 SQ SEQUENCE 83 AA; 8796 MW; 929438A81549DBAC CRC64;

Query Match 8.1%; Score 7; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DEANQRA 79
 Db 67 DEANQRA 73

RESULT 25
 Q8DF43
 ID Q8DF43 PRELIMINARY; PRT; 162 AA.
 AC Q8DF43;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN VV10381.
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016798; AAO08905.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 162 AA; 18029 MW; 65272C082012A474 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 162;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ANQRATK 81
 Db 124 ANQRATK 130

RESULT 26
 Q9SBC2
 ID Q9SBC2 PRELIMINARY; PRT; 170 AA.
 AC Q9SBC2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).
 OS Hamamelis virginiana.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Hamamelidaceae; Hamamelis.
 OX NCBI_TaxID=4397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Szpara M.L.T.;
 RT "Isolation of invertase gene sequences from witch hazel (*Hamamelis*
 RT virginiana)." ;
 RL Thesis (1998), Pennsylvania State University.
 CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 DR EMBL; AF091546; AAC99429.1; -;
 DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR001362; Glyco_hydro_32;
 DR Pfam; PF00251; Glyco_hydro_32; 1-
 DR SMART; SM00640; Glyco_32; 1.
 KW Glycoprotein; Glycosidase; Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 170 170
 SQ SEQUENCE 170 AA; 19356 MW; BE388990C7236D31 CRC64;

Query Match 8.1%; Score 7; DB 10; Length 170;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 IDTQNRQ 57
 Db 67 IDTQNRQ 73

RESULT 27
 Q9ZSW8
 ID Q9ZSW8 PRELIMINARY; PRT; 171 AA.
 AC Q9ZSW8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).
 OS Hamamelis virginiana.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Hamamelidaceae; Hamamelis.
 OX NCBI_TaxID=4397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Szpara M.L.T.;
 RT "Isolation of invertase gene sequences from witch hazel (*Hamamelis*
 RT virginiana)." ;
 RL Thesis (1998), Pennsylvania State University.
 CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
 DR EMBL; AF091545; AAC99428.1; -;
 DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR001362; Glyco_hydro_32;
 DR Pfam; PF00251; Glyco_hydro_32; 1-
 DR SMART; SM00640; Glyco_32; 1.
 KW Glycoprotein; Glycosidase; Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 171 171
 SQ SEQUENCE 171 AA; 19494 MW; B5D4EFB5C0798FEC CRC64;

Query Match 8.1%; Score 7; DB 10; Length 171;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 IDTQNRQ 57
 Db 68 IDTQNRQ 74

RESULT 28

P95796
ID P95796 PRELIMINARY; PRT; 197 AA.
AC P95796;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Serratia marcescens.
OG Plasmid R478.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA Whelan K.F., Bekkering M., Taylor D.E.;
RT "Analysis of the region upstream of terZ in plasmid R478.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59239; AAB37123.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 197 AA; 22154 MW; C98FA5589FC97840 CRC64;

Query Match 8.1%; Score 7; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 RRVNAR 21

Db 150 RRVNAR 156

RESULT 29

O44419
ID O44419 PRELIMINARY; PRT; 212 AA.
AC O44419;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosomal-associated protein 25.
GN SNAP-25.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulz J.R., Sasaki J.D., Vacquier V.D.;
RT "Increased association of synaptosome-associated protein of 25 kDa with syntaxin and vesicle-associated membrane protein following acrosomal exocytosis of sea urchin sperm.";
RL J. Biol. Chem. 273:24355-24359(1998).
DR EMBL; AF036902; AAC35867.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 2.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 212 AA; 24108 MW; 47C1EB69459F250A CRC64;

Query Match 8.1%; Score 7; DB 5; Length 212;

Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMA 44

Db 164 GNLRHMA 170

RESULT 30

O76338
ID O76338 PRELIMINARY; PRT; 212 AA.
AC O76338;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ovarian synaptosome-associated protein 25 homolog.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Tahara M., Coorsen J.R., Timmers K., Blank P.S., Whalley T.,
RT "Calcium can disrupt the SNARE protein complex on sea urchin egg secretory vesicles without irreversibly blocking fusion.";
RL J. Biol. Chem. 273:33667-33673(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Kolosova I.A., Timmers K., Kingsley D.H., Bezrukov L., Zimmerberg J.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF061750; AAC83577.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 2.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 212 AA; 24014 MW; E1B9EDB43C056AD7 CRC64;

Query Match 8.1%; Score 7; DB 5; Length 212;

Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMA 44

Db 164 GNLRHMA 170

RESULT 31

O9CVN5
ID O9CVN5 PRELIMINARY; PRT; 226 AA.
AC O9CVN5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 1700095F04RIK protein (Fragment).
GN 1700095F04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RT STRAIN=C57BL/6J; TISSUE=Testis;
RL MEDLINE=21085660; PubMed=11217851;
DR Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
DR Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
DR Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
DR Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
DR Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
DR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
DR Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
DR Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK007251; BAB24916.1; -
 DR MGD; MGI:1914606; 1700095F04Rik.
 FT NON TER 226 226
 SQ SEQUENCE 226 AA; 26797 MW; 90EAL783E4675997 CRC64;

Query Match 8.1%; Score 7; DB 11; Length 226;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQ 77
 |||||
 Db 41 RIDEANQ 47

RESULT 32

Q8NA63
 ID Q8NA63 PRELIMINARY; PRT; 228 AA.
 AC Q8NA63;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ35807.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
 RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK093126; BAC04065.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 228 AA; 26968 MW; 7F0AFA085E5887D CRC64;

Query Match 8.1%; Score 7; DB 4; Length 228;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQ 77
 |||||
 Db 26 RIDEANQ 32

RESULT 33

Q8N6Q1
 ID Q8N6Q1 PRELIMINARY; PRT; 271 AA.
 AC Q8N6Q1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Similar to RIKEN CDNA 1700095F04 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029221; AAH29221.1; -
 SQ SEQUENCE 271 AA; 32219 MW; 3AB387A2DC398712 CRC64;

Query Match 8.1%; Score 7; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQ 77
 |||||
 Db 9 RIDEANQ 15

RESULT 34

Q926K3
 ID Q926K3 PRELIMINARY; PRT; 285 AA.
 AC Q926K3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein pli0057.
 GN PLI0057.
 OS Listeria innocua.
 OG Plasmid pli100.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Feihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
 DR EMBL; AL592102; CAC42055.1; -
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 285 AA; 32850 MW; 92982A93BD476332 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 285;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIME 63
 |||||
 Db 254 QIDRIME 260

RESULT 35

Q9D9D5
 ID Q9D9D5 PRELIMINARY; PRT; 303 AA.
 AC Q9D9D5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 1700095F04Rik protein (RIKEN CDNA 1700095F04).
 GN 1700095F04Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testicle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testicle;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK007078; BAB24853.1; -;
 DR EMBL; BC049568; AAH49568.1; -;
 DR MGD; MGI:1914606; 1700095F04Rik.
 SQ SEQUENCE 303 AA; 35853 MW; D4AA3952B5C10586 CRC64;

Query Match 8.1%; Score 7; DB 11; Length 303;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQ 77
 Db 41 RIDEANQ 47

RESULT 36
 Q97EN6
 ID Q97EN6 PRELIMINARY; PRT; 350 AA.
 AC Q97EN6;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mannose-1-phosphate guanylyltransferase.
 GN CAC3072.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007804; AAK81012.1; -;
 DR PIR; A97278; A97278.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR005835; NTP transferase.
 DR Pfam; PF00483; NTP transferase; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 KW Transferase; Nucleotidyltransferase; Complete proteome.
 SQ SEQUENCE 350 AA; 39984 MW; 0925415F6152C252 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 350;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 IMEKADS 67
 Db 254 IMEKADS 260

RESULT 37

Q8X9Q9
 ID Q8X9Q9 PRELIMINARY; PRT; 380 AA.
 AC Q8X9Q9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein z1169.
 GN z1169 OR z1608 OR ECS1349.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

```
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005309; AAG55723.1; -.
DR EMBL; AE005273; AAG55314.1; -.
DR EMBL; AP002554; BAB34772.1; -.
DR PIR; E90797; E90797.
DR PIR; G85657; G85657.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 380 AA; 42005 MW; E58261986A615927 CRC64;

Query Match      8.1%; Score 7; DB 16; Length 380;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 RRVTNAR 21
      |||||
Db      150 RRVTNAR 156

RESULT 38
Q836N1
ID Q836N1 PRELIMINARY; PRT; 384 AA.
AC
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Multidrug resistance protein, putative.
GN EF1078.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=225050857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL; AE016950; AAO80880.1; -.
DR TIGR; EF1078; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015520; F:tetracycline:hydrogen antiporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0015904; P:tetracycline transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR InterPro; IPR001958; TCR_TetA.
DR Pfam; PF00083; sugar tr; 1.
DR PRINTS; PR01035; TCR_TETA.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Complete proteome.
SQ SEQUENCE 384 AA; 41284 MW; 67622D55D7196EB8 CRC64;

Query Match      8.1%; Score 7; DB 16; Length 384;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AISGGFI 14
      |||||
Db      138 AISGGFI 144

RESULT 40
Q8GR72
ID Q8GR72 PRELIMINARY; PRT; 393 AA.
AC
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Multidrug efflux pump.
GN EMEA.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29212;
RA Lee E., Kuroda T., Morita Y., Mizushima T., Tsuchiya T.;
RT "Enterococcus faecalis ATCC29212 emeA gene for multidrug resistance
RT pump, complete cds.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091338; BAC11911.1; -.

Query Match      8.1%; Score 7; DB 16; Length 387;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AISGGFI 14
      |||||
Db      138 AISGGFI 144

RESULT 39
Q9CJ77
ID Q9CJ77 PRELIMINARY; PRT; 387 AA.
AC
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Multidrug efflux transporter.
GN BLT OR LL0123.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006250; AAK04221.1; -.
DR PIR; C86640; C86640.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015520; F:tetracycline:hydrogen antiporter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0015904; P:tetracycline transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR InterPro; IPR005829; Sug_transporter.
DR InterPro; IPR001958; TCR_TetA.
DR Pfam; PF00083; sugar tr; 1.
DR PRINTS; PR01035; TCR_TETA.
DR PROSITE; PR01036; TCR_TETB.
DR PROSITE; PS00850; MFS; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
KW Complete proteome.
SQ SEQUENCE 387 AA; 41671 MW; A3E991E0C39C71A6 CRC64;
```

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0015520; F: tetraacycline:hydrogen antiporter activity; IEA.
 DR GO: GO:0005215; F: transporter activity; IEA.
 DR GO: GO:0015904; P: tetraacycline transport; IEA.
 DR GO: GO:0006810; P: transport; IEA.
 DR InterPro: IPR007114; MFS.
 DR InterPro: IPR005828; Sub transporter.
 DR InterPro: IPR005829; Sug transporter.
 DR InterPro: IPR001958; TCR TetA.
 DR Pfam: PF00083; sugar tr; 1.
 DR PRINTS: PR01035; TCR_TET.
 DR PROSITE: PS00850; MFS; 1.
 DR PROSITE: PS00216; SUGAR TRANSPORT 1; 1.
 SQ SEQUENCE 393 AA; 42082 MW; 7614EAFB8A748088 CRC64;

Query Match 8.1%; Score 7; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AISGGFI 14
 |||||
 Db 138 AISGGFI 144

RESULT 41
 Q8U6M7 PRELIMINARY; PRT; 396 AA.
 AC Q8U6M7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein Atu4780.
 GN ATU4780 OR AGR L 206.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328 (2001).
 DR EMBL: AE009406; AAL45574.1; ALT_INIT.
 DR EMBL: AE008208; AAK88669.1; -.
 DR PIR: AH3144; AH3144.
 DR PIR: C98143; C98143.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 396 AA; 40524 MW; 45951BG300A1017A CRC64;

Query Match 8.1%; Score 7; DB 16; Length 396;

Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNL 40
 |||||
 Db 261 SGILGNL 267

RESULT 42
 Q7TV99 PRELIMINARY; PRT; 407 AA.
 AC Q7TV99;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE tRNA-(guanine-N1)-methyltransferase fused to 2-C-methyl-D-erythritol
 DE 2,4-cyclodiphosphate synthase.
 GN TRMD/ISPF OR PRO1354.
 OS Prochlorococcus marinus.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SARG / CCMP 1375 / SS120;
 RX MEDLINE=22810154; PubMed=12917486;
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
 RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
 RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
 RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
 RA Wolf Y.I., Hess W.R.;
 RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
 RT a nearly minimal oxyphototrophic genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).
 DR EMBL: AE017165; AAQ00398.1; -.
 KW Methyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 407 AA; 45243 MW; 59278101AD67707C CRC64;

Query Match 8.1%; Score 7; DB 16; Length 407;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRID 73
 |||||
 Db 234 SNKTRID 240

RESULT 43
 Q93231 PRELIMINARY; PRT; 414 AA.
 AC Q93231;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein C17E4.10.
 GN C17E4.10.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Percy C.M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018 (1998).
 DR EMBL: Z81037; CAB02748.2; -.
 DR PIR: T19354; T19354.


```
DR WormPep; C17E4.10; CE32589.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 414 AA; 47535 MW; 2095705E25CF4C59 CRC64;

Query Match      8.1%; Score 7; DB 5; Length 414;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 ENEEMDE 28
Db 248 ENEEMDE 254

RESULT 44
Q8S0Z9 PRELIMINARY; PRT; 473 AA.
AC Q8S0Z9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P0445E10.22 protein (P0478H03.16 protein).
GN P0445E10.22 OR P0478H03.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0445E10."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0478H03."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003347; BAB86062.1; -.
DR EMBL; AF003452; BAB92700.1; -.
DR Gramene; Q8S0Z9; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:antipporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002528; MatE.
DR Pfam; PF01554; MatE; 2.
DR TIGRFAMs; TIGR00797; matE; 1.
SQ SEQUENCE 473 AA; 51131 MW; 44427CCFA66353FE CRC64;

Query Match      8.1%; Score 7; DB 10; Length 473;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRID 73
Db 437 SNKTRID 443

RESULT 45
Q7SZP4 PRELIMINARY; PRT; 562 AA.
AC Q7SZP4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056314; AAH56314.1; -.
KW Hypothetical protein.
SQ SEQUENCE 562 AA; 64750 MW; 811AA64F5B30F9FB CRC64;

Query Match      8.1%; Score 7; DB 13; Length 562;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 EKADSNK 69
Db 546 EKADSNK 552

Search completed: March 4, 2004, 08:34:12
Job time : 42 secs
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:29:20 ; Search time 14 Seconds
(without alignments)
319.860 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDEREQMAISGFIRRTNA.....SNKTRIDEANQRATKMLGSG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	57.0	204	1 SN2A CARAU	P36977 carassius a
2	49	57.0	206	1 SN25 HUMAN	P13795 homo sapien
3	25	29.1	203	1 SN2B CARAU	P36978 carassius a
4	15	17.4	54	1 SN25 RABIT	P55820 oryctolagus
5	10	11.6	210	1 SN25 TORMA	P36976 torpedo mar
6	8	9.3	212	1 SN25 DROME	P36975 drosophila
7	7	8.1	422	1 EF1A METMA	Q8pur8 methanosarc
8	6	7.0	138	1 C141 HUMAN	Q9y3e0 homo sapien
9	6	7.0	138	1 C141 MOUSE	Q9cr60 mus musculu
10	6	7.0	141	1 MLR4 SCHPO	Q09196 schizosacch
11	6	7.0	147	1 RM28 YEAST	P36527 saccharomyc
12	6	7.0	149	1 ARGR LISIN	Q92by8 listeria in
13	6	7.0	149	1 ARGR LISMO	Q8y7b9 listeria mo
14	6	7.0	152	1 YBE6 PSEAE	Q9hv53 pseudomonas
15	6	7.0	157	1 YGAO BACSU	P97029 bacillus su
16	6	7.0	168	1 YE56 HABIN	P44203 haemophilus
17	6	7.0	175	1 ATPF CHLRE	Q8ht15 chlamydomon
18	6	7.0	178	1 AAC2 PROST	Q52424 providencia
19	6	7.0	199	1 TRPF CAMJE	Q9pif3 campylobact
20	6	7.0	200	1 YE15 HABIN	P44187 haemophilus
21	6	7.0	201	1 CERL HUMAN	Q9ntu7 homo sapien
22	6	7.0	201	1 COAE CLOAB	Q97k22 clostridium
23	6	7.0	225	1 MTRD METKA	Q32864 methanopyru
24	6	7.0	236	1 YW2 YEAST	P40586 saccharomyc
25	6	7.0	238	1 KP5C RAT	P56536 rattus norv
26	6	7.0	242	1 Y22T AGRVI	O34299 agrobacteri
27	6	7.0	245	1 KDSB FUSNN	Q8rfa8 fusobacteri
28	6	7.0	254	1 RPIA TREPA	O83625 treponema p
29	6	7.0	261	1 YRKJ BACSU	P54437 bacillus su
30	6	7.0	269	1 SET DROME	P53997 drosophila
31	6	7.0	271	1 ATPP STAAU	P18179 staphylococ
32	6	7.0	280	1 CTX3 HUMAN	Q9ujq1 homo sapien
33	6	7.0	281	1 PSTA METJA	Q58419 methanococc

34	6	7.0	302	1 RS3 HALNI	P15009 halobacteri
35	6	7.0	304	1 RS3 HALMA	P20281 haloarcula
36	6	7.0	305	1 E2BA HUMAN	Q14232 homo sapien
37	6	7.0	305	1 E2BA MOUSE	Q991c8 mus musculu
38	6	7.0	315	1 GCP MYCGE	P47292 mycoplasma
39	6	7.0	321	1 PDR BURCE	P33164 burkholderi
40	6	7.0	330	1 YC7B SYN3	P74192 synechocyst
41	6	7.0	337	1 YA65 METJA	Q58465 methanococc
42	6	7.0	351	1 MURG HAEIN	P45065 haemophilus
43	6	7.0	352	1 ALR NEIMA	Q9jta6 neisseria m
44	6	7.0	352	1 ALR NEIMB	Q9jyc4 neisseria m
45	6	7.0	383	1 ALR CHLTE	Q8kb67 chlorobium

ALIGNMENTS

RESULT 1
ID SN2A CARAU STANDARD; PRT; 204 AA.
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25A (SNAP-25A).
GN SNAP-A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
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DR EMBL; L22973; AAA16537.1; -.
DR PIR; I50480; I50480.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T SNARE; 2.
KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 85 92 CVS-RICH.
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;

Query Match 57.0%; Score 49; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 156 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 204

RESULT 2
 SN25_HUMAN STANDARD; PRT; 206 AA.
 AC P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
 GN SNAP25 OR SNAP.
 OS Homo sapiens (Human),
 OS Macaca mulatta (Rhesus macaque),
 OS Mus musculus (Mouse),
 OS Rattus norvegicus (Rat), and
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 9544, 10090, 10116, 9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94156217; PubMed=8112622;
 RA Bark I.C., Wilson M.C.;
 RT "Human cDNA clones encoding two different isoforms of the nerve
 RT terminal protein SNAP-25.";
 RL Gene 139:291-292 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94333829; PubMed=8056350;
 RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
 RT "Cloning and sequence analysis of the human SNAP25 cDNA.";
 RL Gene 145:313-314 (1994).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Human; TISSUE=Skeletal muscle;
 RX MEDLINE=96332494; PubMed=8760387;
 RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,
 RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,
 RA Frenkel M.J., Ward C.W.;
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25
 RT (synaptosomal-associated protein 25) A and B isoforms in addition to
 RT syntaxin 4 and synaptobrevins 1 and 2.";
 RL Biochem. J. 317:945-954 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Human; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=M.mulatta; TISSUE=Hippocampus;
 RA Jensen M.J., Smith L.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=BA1B/c;
 RX MEDLINE=90078337; PubMed=2592413;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 RA Bloom F.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein,
 RT SNAP-25, differentially expressed by neuronal subpopulations.";
 RL J. Cell Biol. 109:3039-3052 (1989).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=ILS, and ISS;
 RX MEDLINE=21363810; PubMed=11471062;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 RT "High-throughput sequence identification of gene coding variants
 RT within alcohol-related QTLs.";
 RL Mamm. Genome 12:657-663 (2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempere C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
 RA Strausberg R.L.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Rat;
 RA Kataoka M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Rat; TISSUE=Brain;
 RA Cho A.R., You K.H.;
 RT "Cloning of the SNAP-25 gene from a rat brain cDNA library";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Rat; TISSUE=Brain;
 RX MEDLINE=99155074; PubMed=10037470;
 RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
 RT "SNARE complex proteins, including the cognate pair VAMP-2 and
 RT syntaxin-4, are expressed in cultured oligodendrocytes";
 RL J. Neurochem. 72:988-998 (1999).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken; TISSUE=Retina;
 RX MEDLINE=91126080; PubMed=1992470;
 RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
 RA Wilson M.C.;
 RT "Expression of a conserved cell-type-specific protein in nerve
 RT terminals coincides with synaptogenesis";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789 (1991).
 RN [15]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Chicken;
 RX MEDLINE=93389738; PubMed=8377193;
 RA Bark I.C.;
 RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
 RT encoding distinct isoforms of the protein";
 RL J. Mol. Biol. 233:67-76 (1993).
 RN [16]
 RP PALMITOYLATION.
 RC SPECIES=Rat;
 RX MEDLINE=93100552; PubMed=1281490;
 RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
 RT methionine-rich polypeptide in rapid axonal transport and a major

Query Match 57.0%; Score 49; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.5e-46;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMKADSNKTRIDEANQRATKMLGSG 206
 |||||

RESULT 3
 SN2B_CARAU

ID SN2B_CARAU STANDARD; PRT; 203 AA.
 AC P36978;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25B (SNAP-25B).
 GN SNAP-B.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94068448; PubMed=8248151;
 RA Risinger C., Larhammar D.;
 RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
 RT goldfish";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602 (1993).
 CC -|- FUNCTION: May play an important role in the synaptic function of
 CC specific neuronal systems. Associates with proteins involved in
 CC vesicle docking and membrane fusion.
 CC -|- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 CC the nerve terminal.
 CC -|- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and
 CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
 CC granule cells of the cerebellum.
 CC -|- SIMILARITY: Belongs to the SNAP-25 family.
 CC -|- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC
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 CC
 CC EMBL; L22976; AAA16538.1; -.
 DR PIR; I50481; I50481.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T-SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS50192; T-SNARE; 2.
 KW Synaptosome; Neuron; Repeat; Coiled coil; Multigene family.
 FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
 FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOMOLOGY 2.
 FT DOMAIN 85 92 CYS-RICH.
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 203 AA; 22664 MW; 8DFBBEBED37D6D7 CRC64;
 Query Match 29.1%; Score 25; DB 1; Length 203;
 Best Local Similarity 100.0%; Pred. No. 5.8e-20;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIM 62
 Db 155 GNLRHMDMGNEIDTQNRQIDRIM 179
 |||||

RESULT 4
 SN25_RABIT STANDARD; PRT; 54 AA.
 ID SN25_RABIT
 AC P55820;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP
 DE (Fragments)).

GN SNAP25 OR SNAP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN-New Zealand white; TISSUE=Eye, and Spinal cord;
 RX MEDLINE=92044785; PubMed=1941090;
 RA Loewy A., Liu W.-S., Baitinger C., Willard M.B.;
 RT "The major 35S-methionine-labeled rapidly transported protein
 (superprotein) is identical to SNAP-25, a protein of synaptic
 terminals.";
 RL J. Neurosci. 11:3412-3421(1991).
 CC -!- FUNCTION: tSNARE involved in the molecular regulation of
 synaptic function of specific neuronal systems. Associates with
 proteins involved in vesicle docking and membrane fusion (By
 similarity).
 CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
 and STX1A (By similarity).
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 KW Neurone; Synaptosome.
 FT NON_CONS 29 30
 FT NON_CONS 45 46
 FT NON_CONS 49 50
 SQ SEQUENCE 54 AA; 6064 MW; 00014P740FEB29C5 CRC64;

Query Match 17.4%; Score 15; DB 1; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDREQMAISGGFIR 15
 |||||
 Db 31 VDREQMAISGGFIR 45

RESULT 5
 SN25_TORMA STANDARD; PRT; 210 AA.
 ID SN25_TORMA
 AC P36976;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25).
 OS Torpedo marmorata (Marbled electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hypnosqualea; Pristiogaster; Batoidae;
 OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
 OX NCBI_TaxID=7788;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Electric lobe;
 RX MEDLINE=94043281; PubMed=8226991;
 RA Risinger C., Blomqvist A.G., Lundell I., Larhammar D.,
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.,
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
 (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
 RL J. Biol. Chem. 268:24408-24414(1993).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 specific neuronal systems. Associates with proteins involved in
 vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 the nerve terminal.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC
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 DR EMBL; L22020; AAA49284.1; -.
 DR PIR; I50552; I50552.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T-SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS50192; T-SNARE; 2.
 KW Synaptosome; Neurone; Repeat; Coiled coil.
 FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOMOLOGY 1.
 FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOMOLOGY 2.
 FT DOMAIN 88 96 CYS-RICH.
 SQ SEQUENCE 210 AA; 23652 MW; 58FE471A9234B8B1 CRC64;

Query Match 11.6%; Score 10; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHMLDM 47
 |||||
 Db 165 GNLRHMLDM 174

RESULT 6
 SN25_DROME STANDARD; PRT; 212 AA.
 ID SN25_DROME
 AC P36975;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25).
 GN SNAP25.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=94043281; PubMed=8226991;
 RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.,
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
 (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
 RL J. Biol. Chem. 268:24408-24414(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97417485; PubMed=9272858;
 RA Risinger C., Deitcher D.L., Lundell I., Schwarz T.L., Larhammar D.,
 RT "Complex gene organization of synaptic protein SNAP-25 in Drosophila
 melanogaster.";
 RL Gene 194:169-177(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=22426071; PubMed=12537574;
 RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
 RA Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
 RA Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,
 RA Karpen G.H.;
 RT "Heterochromatic sequences in a Drosophila whole-genome shotgun
 assembly.";
 RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 specific neuronal systems. Associates with proteins involved in
 vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 the nerve terminal.
 CC -!- TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GLANGLIA.

CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L22021; AAB16059.1; -
 CC EMBL; U81153; AAB39757.1; -
 CC EMBL; U81147; AAB39757.1; JOINED.
 CC EMBL; U81148; AAB39757.1; JOINED.
 CC EMBL; U81149; AAB39757.1; JOINED.
 CC EMBL; U81150; AAB39757.1; JOINED.
 CC EMBL; U81151; AAB39757.1; JOINED.
 CC EMBL; U81152; AAB39757.1; JOINED.
 CC FlyBase; FBgn0011288; Snap25.
 CC GO; GO:0005886; C:plasma membrane; NAS.
 CC GO; GO:0005486; F:t-SNARE activity; NAS.
 CC GO; GO:0007269; P:neurotransmitter secretion; NAS.
 CC GO; GO:0016081; P:synaptic vesicle docking; NAS.
 CC GO; GO:0016083; P:synaptic vesicle fusion; NAS.
 CC InterPro; IPR000928; SNAP-25.
 CC InterPro; IPR000727; T-SNARE.
 CC Pfam; PF00835; SNAP-25; 1.
 CC Pfam; PF05739; SNARE; 1.
 CC SMART; SM00397; t-SNARE; 2.
 CC PROSITE; PSS0192; T-SNARE; 2.
 CC Synaptosome; Neurone; Repeat; Coiled coil.
 CC T-SNARE COILED-COIL HOMOMOLOGY 1.
 CC T-SNARE COILED-COIL HOMOMOLOGY 2.
 CC CYS-RICH.
 CC SEQUENCE 212 AA; 23685 MW; BDC90649A1AF3AC8 CRC64;

Query Match 9.3%; Score 8; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QNRQIDRI 61
 |||||
 Db 182 QNRQIDRI 189

RESULT 7
 EF1A_METMA STANDARD; PRT; 422 AA.
 AC Q8PUB8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu).
 GN TUF OR MM2264.
 OS Methanosarcina mazei (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2209;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=22120827; PubMed=12125824;
 RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wier A., Baumer S., Jacobi C.,
 RA Brueggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
 RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Fritz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazei: evidence for lateral gene
 RT transfer between Bacteria and Archaea."
 RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
 CC -!- FUNCTION: This protein promotes the GTP-dependent binding of
 CC aminoacyl-tRNA to the A-site of ribosomes during protein

CC biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-Tu/EF-1A subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE013467; AAM31960.1; -
 CC HAMAP; MF 00118; -; 1.
 CC InterPro; IPR004539; EF1_alpha.
 CC InterPro; IPR000795; EF_GTPbind.
 CC InterPro; IPR004160; EFTU_Cterm.
 CC InterPro; IPR004161; EFTU_D2.
 CC InterPro; IPR009001; Elong_init_C.
 CC InterPro; IPR005225; Small_GTP.
 CC InterPro; IPR009000; Translat_factor.
 CC Pfam; PF00009; GTP_EFTU; 1.
 CC Pfam; PF03144; GTP_EFTU_D2; 1.
 CC Pfam; PF03143; GTP_EFTU_D3; 1.
 CC PRINTS; PR00315; ELONGATNFTCT.
 CC TIGRFAMs; TIGR00483; EF-1_alpha; 1.
 CC TIGRFAMs; TIGR00231; small_GTP; 1.
 CC PROSITE; PS00301; EFACTOR_GTP; 1.
 CC Elongation factor; Protein biosynthesis; GTP-binding;
 CC Complete proteome.
 CC NP_BIND 14 21 GTP (BY SIMILARITY).
 CC NP_BIND 91 95 GTP (BY SIMILARITY).
 CC NP_BIND 146 149 GTP (BY SIMILARITY).
 CC SEQUENCE 422 AA; 46060 MW; 854FAE284F5A87AA CRC64;

Query Match 8.1%; Score 7; DB 1; Length 422;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 EQVSGIL 37
 |||||
 Db 163 EQVSGIL 169

RESULT 8
 CL141_HUMAN STANDARD; PRT; 138 AA.
 AC Q9Y3E0; Q9P1R9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Hypothetical UPF0198 protein CGI-141 (HDCMA39P).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20272150; PubMed=10810093;
 RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
 RT "Identification of novel human genes evolutionarily conserved in
 RT Caenorhabditis elegans by comparative proteomics.";
 RL Genome Res. 10:703-713(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Amigdala;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wienann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;

RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;
RT "A novel gene from human dendritic cell.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the UPF0198 family.
CC -----
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CC -----
DR EMBL; AF151899; AAD34136.1; -.
DR EMBL; AL136571; CAB66506.1; -.
DR EMBL; AF068292; AAF65181.1; ALT_INIT.
DR EMBL; BC012455; AAH12455.1; -.
DR PIR; T46908; T46908.
DR InterPro; IPR007305; Got1.
DR Pfam; PF04178; Got1; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT CONFLICT 37 37 I -> T (IN REF. 3).
SQ SEQUENCE 138 AA; 15426 MW; 2EB8582C34EFAPA CRC64;

Query Match 7.0%; Score 6; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFIRRV 17
Db 107 GFIRRV 112

RESULT 9
C141 MOUSE STANDARD; PRT; 138 AA.
ID C141_MOUSE
AC Q9CR60;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0198 protein CGI-141 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Colon, and Tongue;
RX MEDLINE=22354683; PubMed=12466851;
RA Nikaido I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balzarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrowsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelina A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszewski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the UPF0198 family.
CC -----
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CC -----
DR EMBL; AK018531; BAB31257.2; ALT_INIT.
DR EMBL; AK009991; BAB26630.1; -.
DR MGD; MGI:1914214; CGI-141.
DR InterPro; IPR007305; Got1.
DR Pfam; PF04178; Got1; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 33 53 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
SQ SEQUENCE 138 AA; 15422 MW; 1BE20294C1C670E5 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFIRRV 17
Db 107 GFIRRV 112

RESULT 10
MLR4_SCHPO STANDARD; PRT; 141 AA.
ID MLR4_SCHPO

Q09196;
 16-OCT-2001 (Rel. 40, Created)
 16-OCT-2001 (Rel. 40, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Myosin regulatory light chain cdc4.
 CDC4 OR SPAP83.08.
 Schizosaccharomyces pombe (Fission yeast).
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 NCBI_TaxID=4896;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=95348187; PubMed=7622565;
 McCallum D., Balasubramanian M.K., Pelcher L.E., Hemmingsen S.M.,
 Gould K.L.;
 "Schizosaccharomycetes pombe cdc4+ gene encodes a novel EF-hand protein
 essential for cytokinesis";
 J. Cell Biol. 130:651-660(1995).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=972;
 MEDLINE=21849401; PubMed=11859360;
 Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 Mooney P., Moule S., Murgall K., Murphy L., Niblett D., Odell C.,
 Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 "The genome sequence of Schizosaccharomycetes pombe";
 Nature 415:871-880(2002).
 [3]
 PHOSPHORYLATION.
 MEDLINE=99292733; PubMed=10364209;
 McCallum D., Feoktistova A., Gould K.L.;
 "Phosphorylation of the myosin-II light chain does not regulate the
 timing of cytokinesis in fission yeast";
 J. Biol. Chem. 274:17691-17695(1999).
 [4]
 INTERACTIONS.
 MEDLINE=21101979; PubMed=11087749;
 Desautels M., Den Haese J.P., Slupsky C.M., McIntosh L.P.,
 Hemmingsen S.M.;
 "Cdc4p, a contractile ring protein essential for cytokinesis in
 Schizosaccharomycetes pombe, interacts with a phosphatidylinositol
 4-kinase";
 J. Biol. Chem. 276:5932-5942(2001).
 [5]
 STRUCTURE BY NMR.
 MEDLINE=21101980; PubMed=11087750;
 Slupsky C.M., Desautels M., Huebert T., Zhao R., Hemmingsen S.M.,
 McIntosh L.P.;
 "Structure of Cdc4p, a contractile ring protein essential for
 cytokinesis in Schizosaccharomycetes pombe";
 J. Biol. Chem. 276:5943-5951(2001).

CC -!- FUNCTION: Involved in cytokinesis. Required for the formation and
 CC function of the contractile ring.
 CC -!- SUBUNIT: Binds to myosin II chains myo2 and myo3. Interacts with
 CC vps27 and a PI 4-kinase.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: Phosphorylated on either Ser-2 or Ser-6 but not both.
 CC Phosphorylation is not essential for the function of the protein.
 CC -!- MISCELLANEOUS: In vitro, this chain does not seem to bind calcium.
 CC -!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
 CC -----
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 CC -----
 CC EMBL; L42454; AAA67467.1; -.
 CC EMBL; AL117210; CAB55175.1; -.
 CC PIR; T39245; T39245.
 CC PDB; 1GGW; 21-MAR-01.
 CC GenBank; SPAP83.08; -.
 CC InterPro; IPR002048; EF-hand.
 CC Pfam; PF00036; ehand; 2.
 CC ProDom; PD000012; EF-hand; 2.
 CC SMART; SM00054; EFh; 2.
 CC PROSITE; PS00018; EF HAND; 1.
 CC Myosin; Calcium-binding; Phosphorylation; Cell division; Septation;
 CC 3D-structure.
 CC CA BIND 87 98 EF-HAND (POTENTIAL).
 CC MOD_RES 2 2 PHOSPHORYLATION.
 CC MOD_RES 6 6 PHOSPHORYLATION.
 CC SEQUENCE 141 AA; 15661 MW; 691731DD7C6A68A9 CRC64;
 Query Match 7.0%; Score 6; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 NEEMDE 28
 |||||
 Db 112 NEEMDE 117
 RESULT 11
 RM28_YEAST
 ID RM28_YEAST STANDARD; PRT; 147 AA.
 AC P36527; Q00949;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 60S ribosomal protein L28, mitochondrial precursor (Yml28).
 GN MRPL28 OR YDR462W OR D8035.6.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92269836; PubMed=1588961;
 RA Wang S.S., Stanford D.R., Silvers C.D., Hopper A.K.;
 RT "STP1, a gene involved in pre-tRNA processing, encodes a nuclear
 RT protein containing zinc finger motifs";
 RL Mol. Cell. Biol. 12:2633-2643(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A.,
 RA Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
 RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
 RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
 RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
 RA Winant A., Yelton M., Botstein D., Davis R.W.;
 RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

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RN [3]
RP SEQUENCE OF 27-53 FROM N.A.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: TO S.POMBE SPAC4F8.05C.
CC
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CC
CC EMBL; M88597; AAA35123.1; -.
CC EMBL; U33050; AAB64900.1; -.
CC PIR; S31243; S31243.
CC GerMOnline; 140954; -.
CC SGD; S0002870; MRPL28.
KW Ribosomal protein; Mitochondrion; Transit peptide.
FT TRANSIT 1 26 MITOCHONDRION.
FT CHAIN 27 147 60S RIBOSOMAL PROTEIN L28.
FT CONFLICT 28 29 RT -> IF (IN REF. 3).
FT CONFLICT 33 37 SSLSP -> VILVI (IN REF. 3).
FT CONFLICT 49 49 M -> K (IN REF. 3).
FT CONFLICT 53 53 R -> P (IN REF. 3).
SQ SEQUENCE 147 AA; 17342 MW; 995BBE515A50393D CRC64;

Query Match 7.0%; Score 6; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LEQVSG 35
DB 14 LEQVSG 19

RESULT 12
ARGR LISIN
ID ARGR LISIN STANDARD; PRT; 149 AA.
AC Q92BY8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Arginine repressor.
GN ARGR OR LIN1404.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kruft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordaiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Regulates arginine biosynthesis genes (By similarity).
CC -!- PATHWAY: Arginine biosynthesis; regulation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argR family.
CC
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CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argR family.
CC
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CC
CC EMBL; AL596168; CAC96635.1; -.
CC PIR; AC1608; AC1608.
CC ListList; LIN01404; -.
CC HAMAP; MF_00173; ; 1.
CC InterPro; IPR001669; Arg_repress.
CC Pfam; PF01316; Arg_repressor; 1.
CC Pfam; PF02863; Arg_repressor C; 1.
CC PRINTS; PR01467; ARGREPRESSOR.
CC ProDom; PD007402; Arg_repress; 1.
CC TIGRFAMs; TIGR01529; argR_whole; 1.
KW Transcription regulation; DNA-binding; Trans-acting factor; Repressor;
KW Arginine biosynthesis; Complete proteome.
SQ SEQUENCE 149 AA; 16811 MW; 364222B56ADDE1BF CRC64;

Query Match 7.0%; Score 6; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 NEIDTQ 54
DB 17 NEIDTQ 22

RESULT 13
ARGR LISMO
ID ARGR LISMO STANDARD; PRT; 149 AA.
AC Q8Y7B9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Arginine repressor.
GN ARGR OR LMO1367.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kruft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordaiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Regulates arginine biosynthesis genes (By similarity).
CC -!- PATHWAY: Arginine biosynthesis; regulation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argR family.
CC
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CC -----
DR EMBL; AL591978; CAC99445.1; -.
DR PIR; AG1245; AG1245.
DR ListList; LMO01367; -.
DR HAMAP; MF 00173; -. 1.
DR InterPro; IPR001669; Arg_repress.
DR Pfam; PF01316; Arg_repressor; 1.
DR Pfam; PF02863; Arg_repressor C; 1.
DR PRINTS; PR01467; ARGREPRESSOR.
DR ProDom; PD007402; Arg_repress; 1.
DR TIGRFAMs; TIGR01529; argR whole; 1.
KW Transcription regulation; DNA-binding; Trans-acting factor; Repressor;
KW Arginine biosynthesis; Complete proteome.
SQ SEQUENCE 149 AA; 16778 MW; 25622476E092E1A1 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 NEIDTQ 54
Db 17 NEIDTQ 22

RESULT 14
YB6_PSEAE STANDARD; PRT; 152 AA.
AC Q9HV53;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0090 protein PA4746.
GN PA4746.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -!- SIMILARITY: Belongs to the UPF0090 family.
CC -----
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CC -----
DR EMBL; AB004886; AAG08132.1; -.
DR PIR; AB3053; AB3053.
DR HAMAP; MF 01077; -. 1.
DR InterPro; IPR003728; DUF150.
DR Pfam; PF02576; DUF150; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 152 AA; 17171 MW; 22583E3104CB50AD CRC64;

Query Match 7.0%; Score 6; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QVSGIL 37
Db 58 QVSGIL 63

RESULT 15
YGAO_BACSU STANDARD; PRT; 157 AA.
AC P97029;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical lipoprotein ygaO precursor.
GN YGAO OR BSU08890.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Cummings N.J., Ruiz-Teran F., Connerton I.F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mosati D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL; Z93102; CAB07526.1; -.
DR EMBL; Z99108; CAB12717.1; -.
DR PIR; B69817; B69817.
DR Subtilist; BG12234; ygaO.
DR InterPro; IPR000437; Prok_lipoprot_S.

DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW Hypothetical protein; Transmembrane; Membrane; Lipoprotein; Signal;
KW Complete proteome; Palmitate.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 157 Hypothetical lipoprotein ygaO.
FT TRANSMEM 42 64 Potential.
FT TRANSMEM 98 120 Potential.
FT TRANSMEM 124 146 Potential.
FT LIPID 18 18 N-palmitoyl cysteine (Potential).
FT LIPID 18 18 S-diacylglycerol cysteine (Potential).
SQ SEQUENCE 157 AA; 17773 MW; FE96AE181D784DDB CRC64;

Query Match 7.0%; Score 6; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DEREQ 7
Db 85 DEREQ 90

RESULT 16
YES6 HAEIN STANDARD; PRT; 168 AA.
AC P44203;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H11456.
GN H11456.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).

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DR EMBL; U32823; AAC23106.1; -.
DR PIR; F64030; F64030.
DR TIGR; H11456; -.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 23 47 POTENTIAL.
SQ SEQUENCE 168 AA; 18751 MW; 1A86077999148E9A CRC64;

Query Match 7.0%; Score 6; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 NLEQVS 34
Db 146 NLEQVS 151

RESULT 17
ATPF CHLRE
ID ATPF CHLRE STANDARD; PRT; 175 AA.
AC Q8HTL5; Q9T2G6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ATP synthase B chain (EC 3.6.3.14) (Subunit I).
GN ATPF.
OS Chlamydomonas reinhardtii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RA Rivier C., Rahire M., Rochaix J.-D.;
RT "Chlamydomonas reinhardtii chloroplast atpF gene."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 13-31.
RC STRAIN=cw15;
RX MEDLINE=96128220; PubMed=8543042;
RA Fiedler H.R., Schmid R., Leu S., Shavit N., Strotmann H.;
RT "Isolation of CF0CF1 from Chlamydomonas reinhardtii cw15 and the N-
RT terminal amino acid sequences of the CF0CF1 subunits."
RL FEBS Lett. 377:163-166(1995).
RN [3]
RP COMPLETE PLASTID GENOME.
RX MEDLINE=22305394; PubMed=12417694;
RA Maul J.E., Lilly J.W., Cui L., depamphilis C.W., Miller W.,
RA Harris E.H., Stern D.B.;
RT "The Chlamydomonas reinhardtii plastid chromosome: islands of genes in
RT a sea of repeats."
RL Plant Cell 14:2659-2679(2002).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC core - and CF(0) - the membrane proton channel. CF(1) has five
CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
CC has three main subunits: a, b and c.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -!- SIMILARITY: Belongs to the ATPase B chain family.

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DR EMBL; AY161319; AA041265.1; ALT INIT.
DR EMBL; BK000554; DAA00955.1; ALT INIT.
DR InterPro; IPR002146; ATPsynB/B'sub.
DR Pfam; PF00430; ATP-synt_B; 1.
KW Hydrogen ion transport; Transmembrane; CF(0); Chloroplast.
FT TRANSMEM 20 42 POTENTIAL.
FT CONFLICT 13 13 H -> M (IN REF. 2).
FT CONFLICT 31 31 A -> Y (IN REF. 2).
SQ SEQUENCE 175 AA; 20064 MW; F0FB3D5195C19B34 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 EANQRA 79
Db 62 EANQRA 67


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RESULT 18
AAC2_PROST          STANDARD;          PRT;    178 AA.
ID  AAC2_PROST
AC  Q52424;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Aminoglycoside 2'-N-acetyltransferase (EC 2.3.1.-) (AAC(2')-IA).
GN  AAC.
OS  Providencia stuartii.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Providencia.
OX  NCBI_TaxID=588;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sch75082831A;
RX  MEDLINE=94012520; PubMed=8407825;
RA  Rather P.N., Orosz E., Shaw K.J., Hare R., Miller G.;
RT  "Characterization and transcriptional regulation of the 2'-N-
RT  acetyltransferase gene from Providencia stuartii.";
RL  J. Bacteriol. 175:6492-6498 (1993).
CC  -!- FUNCTION: INVOLVED IN THE O ACETYLATION OF PEPTIDOGLYCAN. IT IS
CC  ALSO CAPABLE OF ACETYLATING AND INACTIVATING CERTAIN
CC  AMINOGLYCOSIDES AND CONFERS HIGH-LEVEL RESISTANCE TO THESE
CC  ANTIBIOTICS WHEN OVEREXPRESSED.
CC  -!- SIMILARITY: BELONGS TO THE AAC(2')-I FAMILY OF ACETYLTRANSFERASES.
CC  -----
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CC  -----
DR  EMBL; L06156; AAA03550.1; -.
DR  PIR; A49899; A49899.
DR  InterPro; IPR000182; GCN5acetyl_trans.
DR  Pfam; PF00583; Acetyltransf; 1.
KW  Antibiotic resistance; Transferase; Acyltransferase.
SQ  SEQUENCE 178 AA; 20087 MW; A7D72B79AF6A9AC9 CRC64;

Query Match          7.0%; Score 6; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  41 RHMALD 46
Db  64 RHMALD 69

RESULT 19
TRPF_CAMJE
ID  TRPF_CAMJE          STANDARD;          PRT;    199 AA.
AC  Q9PIF3;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).
GN  TRPF OR CJ0347.
OS  Campylobacter jejuni.
OC  Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC  Campylobacteraceae; Campylobacter.
OX  NCBI_TaxID=197;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NCTC 11168;
RX  MEDLINE=20150912; PubMed=10688204;
RA  Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA  Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA  Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA  Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA  Whitehead S., Barrell B.G.;
```

```
RT  "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT  reveals hypervariable sequences.";
RL  Nature 403:665-668 (2000).
CC  -!- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-riboseyl)-anthranilate = 1-
CC  (2-carboxyphenylamino)-1-deoxy-D-ribose 5-phosphate.
CC  -!- PATHWAY: Tryptophan biosynthesis; third step.
CC  -!- SIMILARITY: Belongs to the trpF family.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AL139075; CAB74184.1; -.
DR  PIR; B81377; B81377.
DR  HSSP; Q56320; LDL3.
DR  HAMAP; MF_00135; -; 1.
DR  InterPro; IPR001240; PRAI.
DR  Pfam; PF00697; PRAI; 1.
KW  Isomerase; Tryptophan biosynthesis; Complete proteome.
SQ  SEQUENCE 199 AA; 22481 MW; ACBE754AD6E4B877 CRC64;

Query Match          7.0%; Score 6; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  27 DENLEQ 32
Db  62 DENLEQ 67

RESULT 20
YE15_HAEIN
ID  YE15_HAEIN          STANDARD;          PRT;    200 AA.
AC  P44187;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Hypothetical protein HI1415.
GN  HI1415.
OS  Haemophilus influenzae.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Rd / KW20 / ATCC 51907;
RX  MEDLINE=95350630; PubMed=7542800;
RA  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA  Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA  McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA  Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA  Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA  Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA  Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA  Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA  Venter J.C.;
RT  "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT  Rd.";
RL  Science 269:496-512 (1995).
CC  -!- SIMILARITY: SOME, TO MYCOBACTERIOPHAGES D29 AND L5 GP10.
CC  -----
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CC  -----
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DR EMBL; U32821; AAC23066.1; -.
DR PIR; H64028; H64028.
DR HSSP; P23951; 2BAA.
DR TIGR; H1415; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 200 AA; 22895 MW; 42199FDDA4859FBB CRC64;

Query Match 7.0%; Score 6; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SGGFIR 15
| | | | |
Db 51 SGGFIR 56

RESULT 21

CERL HUMAN
ID CERL HUMAN STANDARD; PRT; 201 AA.
AC Q9NTU7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cerebellin-like glycoprotein 1 precursor.
GN CBLNL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SIMILARITY: Contains 1 Clq domain.
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CC
CC EMBL; AL117383; CAB90173.1; -.
CC Genew; HGNC:16231; CBLNL1.
CC InterPro; IPR001073; Clq.
CC InterPro; IPR008983; TNF_like.

DR Pfam; PF00386; Clq; 1.
DR PRINTS; PR00007; COMPLEMTNC1Q.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; FALSE_NEG.
KW Glycoprotein; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 201 CEREBELLIN-LIKE GLYCOPROTEIN 1.
FT DOMAIN 72 201 Clq.
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 201 AA; 21808 MW; 2CC9B6C25A1929B7 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRI 72
| | | | |
Db 87 SNKTRI 92

RESULT 22

COAE CLOAB
ID COAE CLOAB STANDARD; PRT; 201 AA.
AC Q97K22;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase).
GN COAE OR CAC1099.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11456286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatsov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
CC -!- FUNCTION: Catalyzes the phosphorylation of the 3'-hydroxyl group
CC of dephosphocoenzyme A to form coenzyme A (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + dephospho-CoA = ADP + CoA.
CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; fifth (last) step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the coaE family.
CC
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CC
CC EMBL; AE007626; AAK79073.1; -.
CC PIR; F97035; F97035.
CC HAMAP; MF_00376; -; 1.
CC InterPro; IPR001977; Depp_CoAkinase.
CC Pfam; PF01121; CoaE; 1.
CC ProDom; PD003329; Depp_CoAkinase; 1.
CC TIGRFAMs; TIGR00152; TIGR00152; 1.
CC PROSITE; PS01294; COAE; FALSE_NEG.
KW Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
KW Complete proteome.
KW NP BIND 8 15 ATP (POTENTIAL).
FT NP BIND 201 AA; 23395 MW; DF90E0B8E8F3C6D CRC64;
SQ SEQUENCE 201 AA; 23395 MW; DF90E0B8E8F3C6D CRC64;

Query Match 7.0%; Score 6; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIM 62
Db 187 QIDRIM 192

RESULT 23
MTRD_METKA STANDARD; PRT; 225 AA.
AC O32864;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tetrahydromethanopterin S-methyltransferase subunit D (EC 2.1.1.86)
DE (N5-methyltetrahydromethanopterin-coenzyme M methyltransferase subunit D).
DE subunit D).
GN MTRD OR MK0657.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121200; PubMed=9461302;
RA Harms U., Thauer R.K.;
RT "Identification of the active site histidine in the corrinoid protein MtrA of the energy-conserving methyltransferase complex from Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 250:783-788(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -!- FUNCTION: Part of a complex that catalyzes the formation of methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and methyl-tetrahydromethanopterin. This is an energy-conserving, sodium-ion translocating step (By similarity).
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-(methylthio)ethanesulfonate.
CC -!- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC -!- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC, mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the mtrD family.

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EMBL; Y14428; CAA74768.1; -.
EMBL; AB010359; AAM01872.1; -.
HAMAP; MF_01097; -; 1.
InterPro; IPR005779; Met_transD.
Pfam; PF04207; MtrD; 1.
TIGRFAMs; TIGR01112; mtrD; 1.
KW Methanogenesis; One-carbon metabolism; Transferase; Methyltransferase;
KW Transmembrane; Complete proteome.
FT TRANSMEM 5 25 POTENTIAL.

FT TRANSMEM 40 60 POTENTIAL.
FT TRANSMEM 67 87 POTENTIAL.
FT TRANSMEM 132 152 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
FT TRANSMEM 204 224 POTENTIAL.
SQ SEQUENCE 225 AA; 22872 MW; 6FA9546897670D36 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 VSGILG 38
Db 135 VSGILG 140

RESULT 24
YIW2_YEAST STANDARD; PRT; 236 AA.
AC P40586;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 27.4 kDa protein in HYR1 3'region.
GN YIR042C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313266; PubMed=9169870;
RA Churche C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA Moulé S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL Nature 387:84-87(1997).
CC
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EMBL; Z46902; CAA87001.1; -.
PIR; S50347; S50347.
GermOnline; 139754; -.
SGD; S0001481; YIR042C.
InterPro; IPR000182; GCN5acetyl_trans.
Pfam; PF00593; Acetyltransf; 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 27422 MW; 1B33E72F8B7AB1C6 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEAN 76
Db 108 RIDEAN 113

RESULT 25
KF5C_RAT STANDARD; PRT; 238 AA.
ID_KF5C_RAT
AC P56536;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kinesin heavy chain isoform 5C (Kinesin heavy chain neuron-specific
DE 2) (Fragment).
GN KIF5C OR NKHC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC TISSUE=Brain;
RX MEDLINE=98070240; PubMed=9405049;
RA Sack S., Mueller J., Marx A., Thormaehlen M., Mandelkow E.M.,
RA Brady S.T., Mandelkow E.;
RT "X-ray structure of motor and neck domains from rat brain kinesin.";
RL Biochemistry 36:16155-16165(1997).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS).
RX MEDLINE=98088797; PubMed=9428521;
RA Kozielski F., Sack S., Marx A., Thormaehlen M., Schonbrunn E., Biou V.,
RA Thompson A., Mandelkow E.M., Mandelkow E.;
RT "The crystal structure of dimeric kinesin and implications for
microtubule-dependent motility.";
RL Cell 91:985-994(1997).
CC -!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
CC PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
CC CHAINS.
CC -!- DOMAIN: Composed of three structural domains: a large globular N-
CC terminal domain which is responsible for the motor activity of
CC kinesin (it hydrolyzes ATP and binds microtubule), a central
CC alpha-helical coiled coil domain that mediates the heavy chain
CC dimerization; and a small globular C-terminal domain which
CC interacts with other proteins (such as the kinesin light chains),
CC vesicles and membranous organelles.
CC -!- SIMILARITY: Belongs to the kinesin-like protein family. Kinesin
CC subfamily.
DR PDB; 2KIN; 08-APR-98.
DR PDB; 3KIN; 14-OCT-98.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.
DR KW Motor protein; Microtubule; ATP-binding; Coiled coil; 3D-structure.
FT INIT MET 0 0
FT DOMAIN 1 >238 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 173 >238 MICROTUBULE-BINDING.
FT NP BIND 85 92 ATP (BY SIMILARITY).
FT STRAND 4 7
FT STRAND 9 14
FT HELIX 19 23
FT TURN 24 25
FT STRAND 28 28
FT STRAND 30 33
FT TURN 34 36
FT STRAND 37 40
FT TURN 41 42
FT STRAND 46 47
FT STRAND 50 52
FT TURN 54 55
FT HELIX 58 65
FT TURN 66 66
FT HELIX 67 74
FT TURN 75 76
FT STRAND 78 84
FT TURN 87 88
FT HELIX 91 95
FT TURN 96 96
FT STRAND 97 97
FT TURN 99 100
FT TURN 102 104

FT STRAND 105 105
FT HELIX 107 120
FT TURN 121 121
FT TURN 124 125
FT STRAND 126 138
FT TURN 139 140
FT STRAND 141 144
FT TURN 145 146
FT TURN 148 149
FT STRAND 153 153
FT STRAND 155 157
FT TURN 159 160
FT STRAND 163 165
FT TURN 166 167
FT STRAND 171 173
FT HELIX 176 191
FT TURN 192 193
FT HELIX 197 203
FT STRAND 205 216
FT TURN 217 219
FT STRAND 222 231
FT STRAND 237 238
FT NON TER 238 238
SQ SEQUENCE 238 AA; 27034 MW; 7B254F4894E3BC30 CRC64;
Query Match 7.0%; Score 6; DB 1; Length 238;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 MDENLE 31
Db 122 MDENLE 127
RESULT 26
YZ2T AGRVI
ID YZ2T_AGRVI STANDARD; PRT; 242 AA.
AC O34299;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in TAR-II TTUC' 3'region (ORF22) (Fragment).
OS Agrobacterium vitis (Rhizobium vitis).
OG Plasmid pTiAB3.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=373;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB3;
RA Salomone J.-Y., Crouzet P., de Ruffray P., Otten L.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO A.VITIS HYPOTHETICAL 52.8 kDa PROTEIN IN TAR-I
CC TTUC' 3'REGION (AC P70795).
CC -----
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CC -----
DR EMBL; AF010415; AAB67102.1; -.
DR InterPro; IPR002823; DUF112.
DR Pfam; PF01970; DUF112; 1.
KW Hypothetical protein; plasmid.
FT NON TER 1 1
SQ SEQUENCE 242 AA; 25516 MW; 02324E1DACE81B07 CRC64;
Query Match 7.0%; Score 6; DB 1; Length 242;
Best Local Similarity 100.0%; Pred.No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      33 VSGILG 38
Db      159 VSGILG 164

RESULT 27
KDSB_FUSNN STANDARD; PRT; 245 AA.
AC Q8RFA8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) (CMP-KDO
GN synthetase) (CMP-2-keto-3-deoxyoctulosonic acid synthetase) (CKS).
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyrpides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
CC -!- FUNCTION: Activates KDO (a required 8-carbon sugar) for
incorporation into bacterial lipopolysaccharide in Gram-negative
bacteria (by similarity).
CC -!- CATALYTIC ACTIVITY: CTP + 3-deoxy-D-manno-octulosonate =
diphosphate + CMP-3-deoxy-D-manno-octulosonate.
CC -!- PATHWAY: Lipopolysaccharide biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the kdsB family.
CC
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CC
DR EMBL; AE010590; AAL95003.1; -.
DR HAMAP; MF_00057; -.
DR InterPro; IPR003329; Cytidylyl_trans.
DR InterPro; IPR004528; KdsB.
DR Pfam; PF02348; CTP_transf_3; 1.
DR TIGRFAMs; TIGR00466; kdsB; 1.
KW Lipopolysaccharide biosynthesis; Transferase; Nucleotidyltransferase;
KW Complete proteome.
SQ SEQUENCE 245 AA; 28426 MW; C57AFD7227790D98 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 245;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 ENLEQV 33
Db      229 ENLEQV 234

RESULT 28
RPIA_TREPA STANDARD; PRT; 254 AA.
ID RPIA_TREPA
AC O83625;
DT 30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
(PRI).
GN RPIA OR TP0616.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
agent spirochete."
RL Science 281:375-388(1998).
CC -!- CATALYTIC ACTIVITY: D-ribose 5-phosphate = D-ribose 5-phosphate.
CC -!- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
CC -!- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
CC
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CC
DR EMBL; AE001236; AAC65592.1; -.
DR PIR; E71303; E71303.
DR TIGR; TP0616; -.
DR HAMAP; MF_00170; -.
DR InterPro; IPR004788; RpiA.
DR ProDom; PD005813; RpiA; 1.
DR TIGRFAMs; TIGR00021; rpiA; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 254 AA; 27572 MW; 028FACD2FC5F3751 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 254;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      50 EIDTON 55
Db      109 EIDTON 114

RESULT 29
YRKJ_BACSU STANDARD; PRT; 261 AA.
ID YRKJ_BACSU
AC P54437;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein yrkJ.
GN YRKJ OR BSU26490.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=97124195; PubMed=8969508;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
```

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RT      sporulation genes."
RL      Microbiology 142:3103-3111(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98044033; PubMed=9384377;
RA      Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA      Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA      Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA      Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA      Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA      Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA      Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA      Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA      Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA      Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA      Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA      Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA      Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA      Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA      Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA      Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA      Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA      Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA      Presecan E., Fujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA      Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA      Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA      Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA      Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA      Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA      Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA      Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA      Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA      Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT      "The complete genome sequence of the Gram-positive bacterium Bacillus
RT      subtilis."
RL      Nature 390:249-256(1997).
CC      -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC      -----
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Query Match          7.0%; Score 6; DB 1; Length 261;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 33 VSGILG 38

Db 158 VSGILG 163

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RESULT 30
SET_DROME
ID SET DROME STANDARD; PRT; 269 AA.
AC P53997; Q9VFA5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SET protein.
GN SET OR CG4299.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95348188; PubMed=7622566;
RA Kellogg D.R., Kikuchi A., Fugii-Nakata T., Turck C.W., Murray A.W.;
RT "Members of the NAP/SET family of proteins interact specifically with
RT B-type cyclins."
RL J. Cell Biol. 130:661-673(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -|- SUBUNIT: Interacts specifically with B-type cyclins.
CC -|- SIMILARITY: Belongs to the nucleosome assembly protein (NAP)
CC family.
CC -----
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CC -----
DR EMBL; U30470; AAA74264.1; -.
DR EMBL; AE003708; AAF55155.1; -.
DR FlyBase; FBgn0014879; Set.
DR InterPro; IPR002164; NAP_family.
DR Pfam; PF00956; NAP; 1.
FT DOMAIN 230 269 ASP/GLU-RICH (HIGHLY ACIDIC).
FT CONFLICT 15 15 MISSING (IN REF. 1).
SQ SEQUENCE 269 AA; 30994 MW; 05F88C85933BB09 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QVSGIL 37
Db 92 QVSGIL 97

RESULT 31
ATP STAAU STANDARD; PRT; 271 AA.
AC P18179;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Potential ATP-binding protein (ORF 271).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 9789; TRANSPOSOM=Tn552;
RX MEDLINE=91014696; PubMed=2170815;
RA Rowland S.J., Dyke K.G.H.;
RT "Tn552, a novel transposable element from Staphylococcus aureus.";
RL Mol. Microbiol. 4:961-975(1990).
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CC -----
DR EMBL; X52734; CAA36948.1; -.
DR PIR; S11779; S11779.
KW Transposable element; ATP-binding.
FT NP_BIND 34 41 ATP (BY SIMILARITY).
SQ SEQUENCE 271 AA; 31835 MW; 32F6CCEA73911927 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIM 62
Db 241 QIDRIM 246

RESULT 32
CTX3 HUMAN
ID CTX3 HUMAN STANDARD; PRT; 280 AA.
AC Q9UJ01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein C20orf103 precursor.
GN C20ORF103.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Schra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -----
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CC -----
DR EMBL; AL121740; CAB57330.1; -.
DR EMBL; AL031652; CAC18101.1; -.
DR EMBL; BC050727; AAH50727.1; -.

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DR Genew; HGNC:16097; C20orf103.
KW Transmembrane; Signal; Polymorphism.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 280 PROTEIN C20orf103.
FT DOMAIN 30 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 280 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 12 12 D -> G (in dbSNP:2232259).
FT VARIANT 81 81 /FTId=VAR 014401.
FT VARIANT 103 103 I -> V (in dbSNP:2232263).
FT VARIANT 158 158 /FTId=VAR 014402.
FT VARIANT 158 158 Q -> E (in dbSNP:2232264).
FT VARIANT 158 158 /FTId=VAR 014403.
FT VARIANT 158 158 S -> G (in dbSNP:2232266).
FT SEQUENCE 280 AA; 31472 MW; 7D811D7C04EE70B8 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 280;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDREQ 6
Db 227 VDREQ 232

RESULT 33
PSTA_METJA STANDARD; PRT; 281 AA.
AC Q58419;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable phosphate transport system permease protein pstA.
GN PSTA OR MJ1013.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilange A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).
CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family. CystW subfamily.
-----
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DR EMBL; U67544; AAB99017.1; -.
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DR PIR; D64426; D64426.
DR TIGR; MJ1013; -
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR005672; Phosp_transp2.
DR Pfam; PF00528; BPD_transp; 1.
DR TIGRFAMs; TIGR00974; 3a0107a02c; 1.
DR PROSITE; PS0928; ABC_TM1; 1.
KW Transport; Phosphate transport; Transmembrane; Complete proteome.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 107 127 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 194 214 POTENTIAL.
FT TRANSMEM 251 271 POTENTIAL.
SQ SEQUENCE 281 AA; 30248 MW; A807ECBD406DD45E CRC64;

Query Match 7.0%; Score 6; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 RATKML 83
Db 103 RATKML 108

RESULT 34
RS3_HALN1 STANDARD; PRT; 302 AA.
AC P15009; O24784; Q9HPC8;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S3P (HS4) (HHAS3).
GN RPS3P OR VNG1697G.
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and
OS Halobacterium halobium.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091, 2242;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlshroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Edhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=H.halobium;
RX MEDLINE=89248673; PubMed=2470481;
RA Spiridonova V.A., Akhmanova A.S., Kagramanova V.K., Koepke A.K.E.,
RA Mankin A.S.;
RT "Ribosomal protein gene cluster of Halobacterium halobium: nucleotide
RT sequence of the genes coding for S3 and L29 equivalent ribosomal
RT proteins."
RL Can. J. Microbiol. 35:153-159(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=H.halobium;
RX MEDLINE=97031049; PubMed=8876975;
RA Miyokawa T., Urayama T., Shimooka K., Itoh T.;
RT "Organization and nucleotide sequences of ten ribosomal protein genes
RT from the region equivalent to the S10 operon in the archaeobacterium,
RT Halobacterium halobium."
RL Biochem. Mol. Biol. Int. 39:1209-1220(1996).
RN [4]
```

```
RP SEQUENCE OF 1-16 FROM N.A.
RC SPECIES=H.halobium;
RX MEDLINE=89211383; PubMed=2651152;
RA Mankin A.S.;
RT "The nucleotide sequence of the genes coding for the S19 and L22
RT equivalent ribosomal proteins from Halobacterium halobium.";
RL FEBS Lett. 246:13-16(1989).
CC -!- FUNCTION: Binds the lower part of the 30S subunit head (By
CC similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
CC -!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC -----
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CC -----
DR EMBL; AE005077; AAG19942.1; -.
DR EMBL; X14967; CAA33093.1; -.
DR EMBL; AB006961; BAA22276.1; -.
DR PIR; B84322; B84322.
DR PIR; T43822; T43822.
DR HAMAP; MF_01309; -. 1.
DR InterPro; IPR004087; KH dom.
DR InterPro; IPR009019; KH_prok.
DR InterPro; IPR004044; KH_TYPE_2.
DR InterPro; IPR001351; Ribosomal_S3_C.
DR InterPro; IPR005703; S3_euk_arch.
DR Pfam; PF00013; KH; 1.
DR Pfam; PF00189; Ribosomal_S3_C; 1.
DR SMART; SM00322; KH; 1.
DR TIGRFAMs; TIGR01008; rpsC_E_A; 1.
DR PROSITE; PS00823; KH_TYPE_2; 1.
DR PROSITE; PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.
FT DOMAIN 17 86 KH TYPE-2.
FT CONFLICT 32 32 G -> S (IN REF. 2).
SQ SEQUENCE 302 AA; 33071 MW; 4ADB9D430EA4104B CRC64;

Query Match 7.0%; Score 6; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 IDRIIME 63
DB 117 IDRIIME 122

RESULT 35
RS3_HALMA
ID_RS3_HALMA STANDARD; PRT; 304 AA.
AC P20281;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S3P (HmaS3) (HS1).
GN RPS3P.
OS Haloarcula marismortui (Halobacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153945; PubMed=2406244;
RA Arndt E., Kroemer W., Hatakeyama T.;
RT "Organization and nucleotide sequence of a gene cluster coding for
RT eight ribosomal proteins in the archaeobacterium Halobacterium
RT marismortui.";
RT J. Biol. Chem. 265:3034-3039(1990).
```

```
CC -!- FUNCTION: Binds the lower part of the 30S subunit head (By
CC similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
CC -!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC -----
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CC -----
DR EMBL; J05222; AAA86865.1; -.
DR PIR; I35063; R3HS3S.
DR HAMAP; MF_01309; -. 1.
DR InterPro; IPR004087; KH dom.
DR InterPro; IPR009019; KH_prok.
DR InterPro; IPR004044; KH_TYPE_2.
DR InterPro; IPR001351; Ribosomal_S3_C.
DR InterPro; IPR005703; S3_euk_arch.
DR Pfam; PF00013; KH; 1.
DR Pfam; PF00189; Ribosomal_S3_C; 1.
DR SMART; SM00322; KH; 1.
DR TIGRFAMs; TIGR01008; rpsC_E_A; 1.
DR PROSITE; PS00823; KH_TYPE_2; 1.
DR PROSITE; PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding.
FT DOMAIN 17 86 KH TYPE-2.
SQ SEQUENCE 304 AA; 33588 MW; 3E2B8F3C4548E6F5 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 IDRIIME 63
DB 117 IDRIIME 122

RESULT 36
E2BA_HUMAN
ID_E2BA_HUMAN STANDARD; PRT; 305 AA.
AC Q14232;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Translation initiation factor eIF-2B alpha subunit (eIF-2B GDP-GTP
DE exchange factor).
DE EIF2B1 OR EIF2BA.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Torp A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP VARIANT VWM TYR-208.
RX MEDLINE=21823281; PubMed=11835386;
RA van der Knaap M.S., Leegwater P.A.J., Koenst A.A.M., Visser A.,
RA Naidu S., Oudejans C.B.M., Schutgens R.B.H., Pronk J.C.;
RT "Mutations in each of the five subunits of translation initiation
RT factor eIF2B can cause leukoencephalopathy with vanishing white
RT matter.";
RT Ann. Neurol. 51:264-270(2002).
CC -!- FUNCTION: Catalyzes the exchange of eukaryotic initiation factor
CC 2-bound GDP for GTP.
CC -!- SUBUNIT: Complex of five different subunits; alpha, beta, gamma,
CC delta and epsilon.
CC -!- DISEASE: Defects in EIF2B1 are a cause of leukoencephalopathy with
```

CC vanishing white matter (VWM) [MIM:603896]. VWM is a brain disease
 CC that occurs mainly in children. The neurological signs of VWM
 CC include progressive cerebellar ataxia, spasticity, inconstant
 CC optic atrophy and relatively preserved mental abilities. The
 CC disease is chronic-progressive with, in most individuals,
 CC additional episodes of rapid deterioration following febrile
 CC infections or minor head trauma. Head trauma leads only to motor
 CC deterioration, whereas infections with fever may end in coma.
 CC Death occurs after a variable period of a few years to a few
 CC decades, usually following an episode of fever and coma.
 CC -!- SIMILARITY: Belongs to the EIF-2B alpha/beta/delta subunits
 CC family.
 CC
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 CC
 CC EMBL; X95648; CAA64950.1; -.
 CC GenBank; HGNC:3257; EIF2B1.
 CC GK; Q14232; -.
 CC MIM; 606686; -.
 CC MIM; 603896; -.
 CC GO; GO:0008135; F:translation factor activity, nucleic acid b. . .; TAS.
 CC InterPro; IPR000649; IF-2B.
 CC Pfam; PF01008; IF-2B; 1.
 CC Initiation factor; Protein biosynthesis; Disease mutation.
 KW VARIANT 208 N -> Y (in VWM).
 FT /FTID=VAR_015404.
 FT SEQUENCE 305 AA; 33712 MW; 91A915FF1B80B780 CRC64;
 CC
 CC Query Match 7.0%; Score 6; DB 1; Length 305;
 CC Best Local Similarity 100.0%; Pred. No. 62;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 61 IMEKAD 66
 CC |||||
 CC Db 186 IMEKAD 191
 CC
 CC RESULT 37
 CC E2BA_MOUSE
 CC ID E2BA_MOUSE STANDARD; PRT; 305 AA.
 CC AC Q99LC8;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Translation initiation factor eIF-2B alpha subunit (eIF-2B GDP-GTP
 CC exchange factor).
 CC GN EIF2B1.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=22388257; PubMed=12477932;
 CC RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 CC RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 CC RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 CC RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -!- FUNCTION: Catalyzes the exchange of eukaryotic initiation factor
 CC 2-bound GDP for GTP.
 CC -!- SUBUNIT: Complex of five different subunits; alpha, beta, gamma,
 CC delta and epsilon.
 CC -!- SIMILARITY: Belongs to the EIF-2B alpha/beta/delta subunits
 CC family.
 CC
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 CC
 CC EMBL; BC003426; AA03426.1; -.
 CC MGD; MGI:2384802; Eif2b1.
 CC InterPro; IPR000649; IF-2B.
 CC Pfam; PF01008; IF-2B; 1.
 CC Initiation factor; Protein biosynthesis.
 KW SEQUENCE 305 AA; 33816 MW; 9D9ED81F0D9B8411 CRC64;
 CC
 CC Query Match 7.0%; Score 6; DB 1; Length 305;
 CC Best Local Similarity 100.0%; Pred. No. 62;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 61 IMEKAD 66
 CC |||||
 CC Db 186 IMEKAD 191
 CC
 CC RESULT 38
 CC GCP_MYCGE
 CC ID GCP_MYCGE STANDARD; PRT; 315 AA.
 CC AC P47292;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57).
 CC DE (Glycoprotease).
 CC GN GCP OR MG046.
 CC OS Mycoplasma genitalium.
 CC OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 CC OX NCBI_TaxID=2097;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=ATCC 33530 / G-37;
 CC RX MEDLINE=96026346; PubMed=7569993;
 CC RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 CC RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 CC RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
 CC RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 CC RA Tomb J.F., Dougherty B.A., Bitt K.F., Hu P.-C., Lucier T.S.,
 CC RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 CC "The minimal gene complement of Mycoplasma genitalium.";
 CC Science 270:397-403(1995).
 CC -!- FUNCTION: Could be a metalloprotease.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of O-sialoglycoproteins; cleaves
 CC 31-Arg-|-Asp-32 bond in glycophorin A. Does not cleave
 CC unglycosylated proteins, desialylated glycoproteins or
 CC glycoproteins that are only N-glycosylated.
 CC -!- COFACTOR: Zinc (Probable).
 CC -!- SIMILARITY: Belongs to peptidase family M22.
 CC
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DR EMBL; U39684; AAC71262.1; --
 DR PIR; A64205; A64205.
 DR MEROPS; M22.UPW; --
 DR TIGR; MG046; --
 DR InterPro; IPR000905; Peptidase M22.
 DR Pfam; PF00814; Peptidase M22; 1.
 DR PIRSF; PIRSF004537; Osialgic ppts; 1.
 DR PRINTS; PR00789; OSIALOPTASE.
 DR ProDom; PD002367; Peptidase M22; 1.
 DR TIGRFAMS; TIGR00329; gcp; 1.
 DR PROSITE; PS01016; GLYCOPROTEASE; 1.
 KW Hydrolase; Metalloprotease; Zinc; Complete proteome.
 FT METAL 110 110 ZINC (POTENTIAL).
 FT METAL 114 114 ZINC (POTENTIAL).
 SQ SEQUENCE 315 AA; 34708 MW; D186ECD176C4E574 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 NKTRID 73
 |||||
 Db 227 NKTRID 232

RESULT 39

ID_PDR_BURCE STANDARD; PRT; 321 AA.
 AC P33164; Q9ZFR3;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Phthalate dioxygenase reductase (EC 1.-.-.-) (PDR).
 GN OPHAL.
 OS Burkholderia cepacia (Pseudomonas cepacia).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSO1;
 RX MEDLINE=99069326; PubMed=9851995;
 RA Chang H.K., Zylstra G.J.;
 RT "Novel organization of the genes for phthalate degradation from
 RT Burkholderia cepacia DSO1.";
 RL J. Bacteriol. 180:6529-6537(1998).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND PARTIAL SEQUENCE.
 RC STRAIN=DSO1;
 RX MEDLINE=93088078; PubMed=1280857;
 RA Correll C.C., Batie C.J., Ballou D.P., Ludwig M.L.;
 RT "Phthalate dioxygenase reductase: a modular structure for electron
 RT transfer from pyridine nucleotides to [2Fe-2S].";
 RL Science 258:1604-1610(1992).
 CC -|- FUNCTION: COMPONENT OF THE ELECTRON TRANSFER CHAIN INVOLVED IN
 CC PYRIDINE NUCLEOTIDE-DEPENDENT DIHYDROXYLATION OF PHTHALATE.
 CC UTILIZES FMN TO MEDIATE ELECTRON TRANSFER FROM THE TWO-ELECTRON
 CC DONOR, NADH, TO THE ONE-ELECTRON ACCEPTOR, (2FE-2S).
 CC -|- COFACTOR: FMN.
 CC -|- SUBUNIT: Monomer.
 CC -|- SIMILARITY: Belongs to the PDR/vanB family.
 CC -|- SIMILARITY: In the C-terminal section; belongs to the 2Fe2S plant-
 CC type ferredoxin family.
 CC -----

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DR EMBL; AF095748; AAD03550.1; --
 DR PIR; A44230; A44230.
 DR PDB; 2PIA; 15-APR-93.
 DR InterPro; IPR006058; 2Fe2S fd BS.
 DR InterPro; IPR008333; FAD_binding_6.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001433; Oxired_FAD/NAD(P).
 DR InterPro; IPR000951; Phdiox_reductase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PRINTS; PR00409; PHDIOXRDTASE.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
 KW Oxidoreductase; Flavoprotein; FMN; NAD; Metal-binding; Iron-sulfur;
 FT INIT MET 0 0
 FT NP_BIND 1 102 FMN.
 FT NP_BIND 112 226 NAD.
 FT METAL 272 272 IRON-SULFUR (2FE-2S).
 FT METAL 277 277 IRON-SULFUR (2FE-2S).
 FT METAL 280 280 IRON-SULFUR (2FE-2S).
 FT METAL 308 308 IRON-SULFUR (2FE-2S).
 FT TURN 3 7
 FT STRAND 9 20
 FT TURN 21 22
 FT STRAND 23 29
 FT TURN 31 32
 FT TURN 41 42
 FT STRAND 44 48
 FT TURN 50 51
 FT STRAND 54 58
 FT TURN 63 64
 FT STRAND 68 74
 FT TURN 77 78
 FT HELIX 82 88
 FT TURN 92 93
 FT STRAND 95 98
 FT STRAND 102 102
 FT TURN 109 110
 FT STRAND 113 119
 FT HELIX 120 122
 FT HELIX 123 136
 FT STRAND 140 147
 FT HELIX 150 152
 FT TURN 154 155
 FT HELIX 156 160
 FT TURN 162 167
 FT STRAND 168 172
 FT TURN 174 175
 FT TURN 177 178
 FT HELIX 183 187
 FT TURN 192 193
 FT STRAND 194 199
 FT HELIX 202 211
 FT TURN 212 214
 FT TURN 217 218
 FT STRAND 220 223
 FT STRAND 238 242
 FT TURN 243 245
 FT STRAND 248 251
 FT TURN 253 254
 FT HELIX 257 263
 FT TURN 264 265
 FT TURN 279 280
 FT STRAND 281 286
 FT STRAND 289 290
 FT TURN 298 303
 FT STRAND 304 306

FT TURN 307 309
 FT STRAND 311 312
 FT STRAND 316 319
 SQ SEQUENCE 321 AA; 35533 MW; 84E179CED060D85F CRC64;

Query Match 7.0%; Score 6; DB 1; Length 321;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TNAREN 23
 |||||
 Db 230 TNAREN 235

RESULT 40

YC78 SINY3
 ID YC78 SINY3 STANDARD; PRT; 330 AA.
 AC P74192;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein slr1278.
 GN SLR1278.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- SIMILARITY: BELONGS TO THE UPF0072 (MESJ/YCF62) FAMILY.

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 CC -----

DR EMBL; D90913; BAA18281.1; -.
 DR PIR; S75822; S75822.
 DR InterPro; IPR000541; UPF0021.
 DR Pfam; PF01171; ATP_bind3; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 330 AA; 37771 MW; C7672AC09596E723 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LEQVSG 35
 |||||
 Db 239 LEQVSG 244

RESULT 41

YA65 METUA
 ID YA65 METUA STANDARD; PRT; 337 AA.
 AC Q58465;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein MJ1065.
 GN MJ1065.

OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii";
 RL Science 273:1058-1073(1996).
 CC -!- SIMILARITY: STRONG, TO B.SUBTILIS SPSE.
 CC -!- SIMILARITY: Contains 1 AFP-like domain.

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 CC -----

DR EMBL; U67549; AAB99068.1; -.
 DR PIR; H64432; H64432.
 DR TIGR; MJ1065; -.
 DR InterPro; IPR006014; Antifreeze dom.
 DR InterPro; IPR006190; Antifreeze_like.
 DR InterPro; IPR004144; NeuB.
 DR Pfam; PF01354; Antifreeze; 1.
 DR Pfam; PF03102; NeuB; 1.
 DR PROSITE; PS50844; AFP LIKE; 1.
 DR KW Hypothetical protein; Complete proteome.
 FT DOMAIN 279 337 AFP-LIKE.
 SQ SEQUENCE 337 AA; 37976 MW; 790CCAPF48C1111B CRC64;

Query Match 7.0%; Score 6; DB 1; Length 337;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KMLGSG 86
 |||||
 Db 256 KMLGSG 261

RESULT 42

MURG HAEIN
 ID MURG HAEIN STANDARD; PRT; 351 AA.
 AC P45055;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide)
 DE pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
 DE (EC 2.4.1.227) (Undecaprenyl-PP-MurNAC-pentapeptide-UDPGlcNAc GlcNAc
 DE transferase).
 GN MURG OR H11138.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,


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RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: Cell wall formation. Catalyzes the transfer of a GlcNAc
CC subunit on undecaprenyl-pyrophosphoryl-MurNAc-pentapeptide (lipid
CC intermediate I) to form undecaprenyl-pyrophosphoryl-MurNAc-
CC (pentapeptide)GlcNAc (lipid intermediate II) (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + Mur2Ac(oyl-L-Ala-
CC gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP +
CC GlcNAc-(1->4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-
CC diphosphoundecaprenol.
CC -!- PATHWAY: Peptidoglycan biosynthesis; last step.
CC -!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 28. MurG
CC subfamily.
CC -----
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CC -----
DR EMBL; U32793; AAC22793.1; -.
DR PIR; D64185; D64185.
DR HSSP; P17443; 1F0K.
DR TIGR; H11138; -.
DR HAMAP; MF_00033; -.
DR InterPro; IPR007235; Glyco_tran_28_C.
DR InterPro; IPR004276; Glyco_trans_28.
DR InterPro; IPR006009; MurG.
DR Pfam; PF04101; Glyco_tran_28_C; 1.
DR Pfam; PF03033; Glyco_transf_28; 1.
DR TIGRFAMs; TIGR01133; murG; 1.
KW Transferase; Glycosyltransferase; Cell division; Cell wall; Membrane;
KW Inner membrane; Peptidoglycan synthesis; Complete proteome.
SQ SEQUENCE 351 AA; 38307 MW; 41067F379BB30B27 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ENLEQV 33
Db 230 ENLEQV 235

RESULT 43
ALR_NEIMA STANDARD; PRT; 352 AA.
ID ALR_NEIMA
AC Q9JTA6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
GN ALR OR NMA1906.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
```

```
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
CC -!- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
CC step.
CC -!- SIMILARITY: Belongs to the alanine racemase family.
CC -----
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CC -----
DR EMBL; AL162757; CAB85127.1; -.
DR PIR; B81818; B81818.
DR HSSP; P10724; 1BD0.
DR HAMAP; MF_01201; -.
DR InterPro; IPR000821; Ala_racemase.
DR InterPro; IPR009006; Racem_decarbox_C.
DR InterPro; IPR001608; UPF0001.
DR Pfam; PF00842; Ala_racemase_C; 1.
DR Pfam; PF01168; Ala_racemase_N; 1.
DR PRINTS; PR00992; ALARACEMASE.
DR TIGRFAMs; TIGR00492; alr; 1.
DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
KW Complete proteome.
FT ACT_SITE 33 33 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
FT ACT_SITE 250 250 SIMILARITY).
FT BINDING 33 33 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY
FT BINDING 352 AA; 38848 MW; B595D0B0F3D6ADD5 CRC64; SIMILARITY).
SQ SEQUENCE 352 AA; 38848 MW; B595D0B0F3D6ADD5 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 LGNLRH 42
Db 10 LGNLRH 15

RESULT 44
ALR_NEIMB STANDARD; PRT; 352 AA.
ID ALR_NEIMB
AC Q9JYC4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
GN ALR OR NMB1651.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
```

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RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittance H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -!- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
CC step.
CC -!- SIMILARITY: Belongs to the alanine racemase family.
CC -----
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CC -----
DR EMBL; AE002515; AAF42000.1; -.
DR PIR; B81059; B81059.
DR HSSP; P10724; 1BD0.
DR TIGR; NMB1651; -.
DR HAMAP; MF_01201; -.
DR InterPro; IPR000821; Ala_racemase.
DR InterPro; IPR009006; Racem decarbox_C.
DR InterPro; IPR001608; UPF0001.
DR Pfam; PF00842; Ala_racemase_C; 1.
DR Pfam; PF01168; Ala_racemase_N; 1.
DR PRINTS; PR00992; ALARACEMASE.
DR TIGRFAMs; TIGR00492; alr; 1.
DR PROSITE; PS00395; ALANINE RACEMASE; 1.
KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
KW Complete proteome.
FT ACT_SITE 33 33 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
FT SIMILARITY).
FT ACT_SITE 250 250 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY
FT SIMILARITY).
FT BINDING 33 33 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 352 AA; 38820 MW; 0AC586A9E12860E6 CRC64;
Query Match 7.0%; Score 6; DB 1; Length 352;
Best Local Similarity 100.0%; Pred.No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 LGNLRH 42
Db 10 LGNLRH 15
RESULT 45
ALR_CHLTE STANDARD; PRT; 383 AA.
AC Q8XB67;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
GN ALR OR CT1922.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;

```

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RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., DeBoy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Niernan W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
CC -!- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
CC step.
CC -!- SIMILARITY: Belongs to the alanine racemase family.
CC -----
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CC -----
DR EMBL; AE012943; AAM73141.1; -.
DR TIGR; CT1922; -.
DR HAMAP; MF_01201; -.
DR InterPro; IPR000821; Ala_racemase.
DR InterPro; IPR009006; Racem decarbox_C.
DR InterPro; IPR001608; UPF0001.
DR Pfam; PF00842; Ala_racemase_C; 1.
DR Pfam; PF01168; Ala_racemase_N; 1.
DR PRINTS; PR00992; ALARACEMASE.
DR TIGRFAMs; TIGR00492; alr; 1.
DR PROSITE; PS00395; ALANINE RACEMASE; 1.
KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
KW Complete proteome.
FT ACT_SITE 50 50 CATALYTIC BASE SPECIFIC TO D-ALANINE
FT (BY SIMILARITY).
FT ACT_SITE 279 279 CATALYTIC BASE SPECIFIC TO L-ALANINE
FT (BY SIMILARITY).
FT BINDING 50 50 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 383 AA; 40986 MW; B41AF5C33872DEC CRC64;
Query Match 7.0%; Score 6; DB 1; Length 383;
Best Local Similarity 100.0%; Pred.No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 LGNLRH 42
Db 25 LGNLRH 30
Search completed: March 4, 2004, 08:33:19
Job time : 15 secs

```

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:31:05 ; Search time 21 Seconds
(without alignments)
393.927 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDREQMAISGGFIRRVINA.....SNKTRIDEANQRATKMLGSG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	49	57.0	204	2 I50480	synapse protein SN
2	49	57.0	206	2 A37861	synaptosomal-assoc
3	49	57.0	206	2 I53735	nerve terminal pro
4	49	57.0	206	2 I67823	nerve terminal pro
5	49	57.0	206	2 A33623	synaptosomal-assoc
6	27	31.4	249	2 S38308	SNAP-25 protein -
7	27	31.4	249	2 S38309	SNAP-25 protein -
8	25	29.1	203	2 I50481	synapse protein SN
9	15	17.4	16	2 A44823	synaptosomal-assoc
10	15	17.4	46	2 S32362	SNAP receptor - bo
11	12	14.0	56	2 S36812	probable synapse-a
12	11	12.8	29	2 A49708	synaptosomal-assoc
13	10	11.6	210	2 I50552	synapse protein -
14	10	11.6	210	2 JC5512	SNARE protein 23 -
15	8	9.3	357	2 H89819	conserved hypothet
16	8	9.3	593	2 H64529	hypothetical prote
17	7	8.1	350	2 A97278	mannose-1-phosphat
18	7	8.1	362	2 AH3144	conserved hypothet
19	7	8.1	380	2 E90797	hypothetical prote
20	7	8.1	380	2 G85657	hypothetical prote
21	7	8.1	386	2 T19354	hypothetical prote
22	7	8.1	387	2 C86640	multidrug efflux t
23	7	8.1	396	2 C98143	hypothetical prote
24	7	8.1	875	2 T45813	hypothetical prote
25	7	8.1	1643	2 T05647	hypothetical prote
26	7	8.1	1711	2 T06119	hypothetical prote
27	7	8.1	1750	2 E86151	hypothetical prote
28	7	8.1	1793	2 T47897	guanine nucleotide
29	6	7.0	75	2 T42409	FMRFamide-like pep

30 6 7.0 84 2 AH3402 hypothetical cytos
31 6 7.0 106 2 T26263 FMRFamide-like pep
32 6 7.0 111 2 T40946 60s ribosomal prot
33 6 7.0 118 2 T17380 vrlA protein - Dic
34 6 7.0 120 2 D82022 truncated pilin NM
35 6 7.0 124 2 E89984 hypothetical prote
36 6 7.0 127 2 AH3491 hypothetical cytos
37 6 7.0 138 2 T46908 hypothetical prote
38 6 7.0 141 2 T39245 ef-hand protein -
39 6 7.0 143 2 C44259 kinesin heavy chai
40 6 7.0 147 2 S31243 ribosomal protein
41 6 7.0 148 2 G95210 acetyltransferase,
42 6 7.0 148 2 A98075 conserved hypothet
43 6 7.0 149 2 AC1608 arginine repressor
44 6 7.0 149 2 AG1245 arginine repressor
45 6 7.0 152 2 A83053 conserved hypothet

ALIGNMENTS

RESULT 1

I50480
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50480
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50480
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-204 <RIS>
A:Cross-references: GB:L22973; NID:G349426; PIDN:AAI6537.1; PID:G349427
C:Genetics:
A:Gene: SNAP-25

Query Match 57.0%; Score 49; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
DB 156 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 204

RESULT 2

A37861
synaptosomal-associated 25K protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
C:Accession: A37861
R:Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coinci
A:Reference number: A37861; MUID:91126080; PMID:1992470
A:Accession: A37861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <CAT>
A:Cross-references: GB:M57957; NID:G212673; PIDN:AAA49072.1; PID:G212674

Query Match 57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
DB 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

```
RESULT 3
I53735
C:Species: Homo sapiens (human)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I53735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I53735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:L19760; NID:g307425; PIDN:AAC37545.1; PID:g307426
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match      57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38  GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db      158  GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 4
I67823
C:Species: Homo sapiens (human)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I67823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I67823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:L19761; NID:g307427; PIDN:AAC37546.1; PID:g307428
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match      57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38  GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db      158  GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 5
A33623
C:Species: Mus musculus (house mouse)
C:Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A33623
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.;
J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differ
A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <OYL>
A:Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998
```

```
Query Match      57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38  GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db      158  GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 6
S38308
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38308
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding di
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38308
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match      31.4%; Score 27; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.2e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38  GNLRHMLDMGNEIDTQNRQIDRIMEK 64
Db      158  GNLRHMLDMGNEIDTQNRQIDRIMEK 184

RESULT 7
S38309
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38309
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding di
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38309
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match      31.4%; Score 27; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.2e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38  GNLRHMLDMGNEIDTQNRQIDRIMEK 64
Db      158  GNLRHMLDMGNEIDTQNRQIDRIMEK 184

RESULT 8
I50481
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50481
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
```

A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: GB:L22976; NID:G349430; PIDN:AA16538.1; PID:G349431
C;Genetics:
A;Gene: SNAP-25

Query Match 29.1%; Score 25; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 7e-19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHMDMGNEIDTQNRQIDRM 62
|||||
Db 155 GNLRHMDMGNEIDTQNRQIDRM 179

RESULT 9
A44823
synaptosomal-associated protein SNAP-25 peptide 10B - rabbit (fragment)
N;Alternate names: superprotein peptide 10B
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: A44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A;Reference number: A44823; MUID:92044785; PMID:1941090
A;Accession: A44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <LOE>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64256)
C;Keywords: membrane trafficking

Query Match 17.4%; Score 15; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDREQMAISGGFIR 15
|||||
Db 2 VDREQMAISGGFIR 16

RESULT 10
S32362
SNAP receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S32362
R;Soellner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromanos, S.; Tem
Nature 362, 318-324, 1993
A;Title: SNAP receptors implicated in vesicle targeting and fusion.
A;Reference number: S32360; MUID:93205116; PMID:8455717
A;Accession: S32362
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-46 <SOE>

Query Match 17.4%; Score 15; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 8.1e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 HMDMGNEIDTQNR 56
|||||
Db 32 HMDMGNEIDTQNR 46

RESULT 11
S36812
probable synapse-associated 28K protein - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: S36812
R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A;Reference number: S36811; MUID:93374072; PMID:8365494
A;Accession: S36812
A;Molecule type: protein
A;Residues: 1-56 <HOR>
A;Experimental source: brain

Query Match 14.0%; Score 12; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AISGGFIRVTN 19
|||||
Db 35 AISGGFIRVTN 46

RESULT 12
A49708
synaptosomal-associated 25K protein - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
C;Accession: A49708
R;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.;
J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulin neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
A;Accession: A49708
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-29 <BIN>

Query Match 12.8%; Score 11; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 IMEXADSNKTR 71
|||||
Db 11 IMEXADSNKTR 21

RESULT 13
I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50552
R;Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) si
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: GB:L22020; NID:G431296; PIDN:AAA49284.1; PID:G431297

Query Match 11.6%; Score 10; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHMDLM 47
|||||
Db 165 GNLRHMDLM 174

RESULT 14
JC5512
SNARE protein 23 - mouse

C;Species: Mus musculus (house mouse)
 C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
 C;Accession: JC5512
 R;Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Oka
 Biochem. Biophys. Res. Commun. 234, 257-262, 1997
 A;Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
 A;Reference number: JC5512; MUID:97312558; PMID:9168999

A;Accession: JC5512
 A;Molecule type: mRNA

A;Residues: 1-210 <ARA>
 A;Cross-references: DDBJ:AB000822; NID:g2189950; PIDN:BAA20345.1; PID:dl021177; PID:g218
 C;Comment: This protein is involved in the insulin-induced translocation of vesicles con

Query Match 11.6%; Score 10; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.0064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MALDMGNEID 52
 |||||
 Db 168 MALDMGNEID 177

RESULT 15

H89819
 conserved hypothetical protein SA0485 [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C;Accession: H89819
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: H89819

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-357 <KUR>

A;Cross-references: GB:BA000018; PID:gl3700417; PIDN:BAB41715.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0485

C;Superfamily: conserved hypothetical protein yacI

Query Match 9.3%; Score 8; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FIRRVTNA 20
 |||||
 Db 60 FIRRVTNA 67

RESULT 16

H64529

hypothetical protein HP0080 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C;Accession: H64529

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: H64529

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-593 <TOM>

A;Cross-references: GB:AE000529; GB:AE000511; NID:g2313152; PIDN:AAD07151.1; PID:g231316

Query Match

9.3%; Score 8; DB 2; Length 593;

Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNLR 41
 |||||
 Db 81 SGILGNLR 88

RESULT 17

A97278

mannose-1-phosphate guanylyltransferase [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: A97278

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: A97278

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-350 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK81012.1; PID:gl5026135; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC3072

Query Match

8.1%; Score 7; DB 2; Length 350;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 IMEXADS 67
 |||||
 Db 254 IMEXADS 260

RESULT 18

AH3144

conserved hypothetical protein Atu4780 [imported] - Agrobacterium tumefaciens (strain C5

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C;Accession: AH3144

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AH3144

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-362 <KUR>

A;Cross-references: GB:AE008689; PIDN:AAL45574.1; PID:gl7743290; GSPDB:GN00187

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu4780

A;Map position: linear chromosome

Query Match

8.1%; Score 7; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNL 40
 |||||
 Db 227 SGILGNL 233

RESULT 19

E90797

hypothetical protein ECs1349 [imported] - Escherichia coli (strain O157:H7, substrain R

C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Nov-2003
C;Accession: E90797
R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90797
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA834772.1; PID:gl3350809; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1349
C;Superfamily: uncharacterized conserved protein

Query Match 8.1%; Score 7; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RRVTNAR 21
|||
Db 150 RRVTNAR 156

RESULT 20
G85657
hypothetical protein Z1608 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Nov-2003
C;Accession: G85657; F85606
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85657
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <STO>
A;Cross-references: GB:AE005174; NID:gl2514491; PIDN:AAG55723.1; GSPDB:GN00145; UWGP:Z16
A;Experimental source: strain O157:H7, substrain EDL933
A;Accession: F85606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <ST2>
A;Cross-references: GB:AE005174; NID:gl2513974; PIDN:AAG55314.1; GSPDB:GN00145; UWGP:Z11
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1169
C;Superfamily: uncharacterized conserved protein

Query Match 8.1%; Score 7; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 RRVTNAR 21
|||
Db 150 RRVTNAR 156

RESULT 21
T19354
hypothetical protein C17E4.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19354
R;Percy, C.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19113
A;Accession: T19354

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-386 <WIL>
A;Cross-references: EMBL:Z81037; PIDN:CAB02748.1; GSPDB:GN00019; CESP:C17E4.10
A;Experimental source: clone C17E4
C;Genetics:
A;Gene: CESP:C17E4.10
A;Map position: 1
A;Introns: 36/3; 98/2; 264/3; 309/2

Query Match 8.1%; Score 7; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 ENEEMDE 28
|||
Db 248 ENEEMDE 254

RESULT 22
C86640
multidrug efflux transporter blt [imported] - Lactococcus lactis subsp. lactis (strain I
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: C86640
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <STO>
A;Cross-references: GB:AE005176; PID:gl2722970; PIDN:AAK04221.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: blt

Query Match 8.1%; Score 7; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AISGGFI 14
|||
Db 138 AISGGFI 144

RESULT 23
C98143
hypothetical protein AGR_L206 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: C98143
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C98143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88669.1; PID:gl15158398; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L206
A;Map position: linear chromosome

Query Match 8.1%; Score 7; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 SGILGNL 40
|||

Db 261 SGILGNL 267

RESULT 24
T45813
hypothetical protein F2809.200 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 23-Mar-2001
C:Accession: T45813
R;Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23014
A:Accession: T45813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-875 <BEV>
A:Cross-references: EMBL:AL137080
A:Experimental source: cultivar Columbia; BAC clone F2809
C:Genetics:
A:Map position: 3
A:Introns: 48/2; 78/2; 100/3; 120/3; 150/3; 236/3; 268/3; 313/3; 331/3; 359/3; 378/3; 67
A:Note: F2809.200
C:Superfamily: Arabidopsis thaliana hypothetical protein At2g41620

Query Match 8.1%; Score 7; DB 2; Length 875;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 RQIDRIM 62
Db 432 RQIDRIM 438

RESULT 25
T05647
hypothetical protein F20D10.320 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T05647
R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15420
A:Accession: T05647
A:Molecule type: DNA
A:Residues: 1-1643 <BEV>
A:Cross-references: EMBL:AL035538
A:Experimental source: cultivar Columbia; BAC clone F20D10
C:Genetics:
A:Map position: 4
A:Introns: 328/3; 444/2; 555/3; 696/3; 734/1; 819/3; 830/3; 994/2; 1101/3; 1222/1; 1442/
A:Note: F20D10.320

Query Match 8.1%; Score 7; DB 2; Length 1643;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 IDRIMEK 64
Db 649 IDRIMEK 655

RESULT 26
T06119
hypothetical protein F23E12.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
C:Accession: T06119
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Hoheisel,
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15485
A:Accession: T06119
A:Molecule type: DNA
A:Residues: 1-1711 <BEV>

A:Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.60
A:Experimental source: cultivar Columbia; BAC clone F23E12
C:Genetics:
A:Gene: ATSP:F23E12.60
A:Map position: 4
A:Introns: 454/2; 572/3; 713/3; 811/2; 902/3; 1068/2; 1175/3; 1294/1; 1512/3

Query Match 8.1%; Score 7; DB 2; Length 1711;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 IDRIMEK 64
Db 666 IDRIMEK 672

RESULT 27
E86151
hypothetical protein F22M8.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86151
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86151
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1750 <STO>
A:Cross-references: GB:AE005172; NID:g8570447; PIDN:AAF76474.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 8.1%; Score 7; DB 2; Length 1750;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 IDRIMEK 64
Db 707 IDRIMEK 713

RESULT 28
T47897
guanine nucleotide exchange factor-like protein - Arabidopsis thaliana
N:Alternate names: protein T4C21.270
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47897
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; S.
.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24479
A:Accession: T47897
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1793 <CHO>
A:Cross-references: EMBL:AL162295
A:Experimental source: cultivar Columbia; BAC clone T4C21
C:Genetics:
A:Map position: 3
A:Introns: 401/2; 507/2; 622/3; 763/3; 861/2; 952/3; 1119/2; 1226/3; 1353/1; 1585/3
A:Note: T4C21.270

Query Match 8.1%; Score 7; DB 2; Length 1793;

Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 IDRIKEX 64
|||||
Db 716 IDRIKEX 722

RESULT 29
T42409
PMRFamide-like peptide 2b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T42409
R;Li, C.; Nelson, L.S.; Memmott, J.M.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z22162
A;Accession: T42409
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-75 <LIC>
A;Cross-references: EMBL:AF042388; PIDN:AAC08939.1
C;Genetics:
A;Gene: flp-2b

Query Match 7.0%; Score 6; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QVSGIL 37
|||||
Db 2 QVSGIL 7

RESULT 30
AH3402
hypothetical cytosolic protein BMEI1206 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3402
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3402
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-84 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52387.1; PID:gl7983187; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1206
A;Map position: I

Query Match 7.0%; Score 6; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 LDMGNE 50
|||||
Db 41 LDMGNE 46

RESULT 31
T26263
PMRFamide-like peptide 2a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T26263; T42408
R;Mortimore, B.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z20185

A;Accession: T26263
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-106 <WIL>
A;Cross-references: EMBL:Z49868; PIDN:CAA90031.1; GSPDB:GN00028; CESP:W07E11.3
A;Experimental source: clone W07E11
R;Li, C.; Nelson, L.S.; Memmott, J.M.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z22162
A;Accession: T42408
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-106 <LIC>
A;Cross-references: EMBL:AF042387; PIDN:AAC08938.1
C;Genetics:
A;Gene: flp-2a; W07E11.3a
A;Map position: X
A;Introns: 92/2

Query Match 7.0%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QVSGIL 37
|||||
Db 2 QVSGIL 7

RESULT 32
T40946
60s ribosomal protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T40946
R;Lucas, M.; Gaillardin, C.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: Z21959
A;Accession: T40946
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-111 <LUC>
A;Cross-references: EMBL:AL035259; PIDN:CAA22868.1; GSPDB:GN00068; SPDB:SPCC1322.15
A;Experimental source: strain 972h; cosmid c1322
C;Genetics:
A;Gene: SPDB:SPCC1322.15
A;Map position: 3
C;Superfamily: rat ribosomal protein L34

Query Match 7.0%; Score 6; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRI 72
|||||
Db 17 SNKTRI 22

RESULT 33
TI7380
vrlA protein - Dichelobacter nodosus
C;Species: Dichelobacter nodosus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: TI7380
R;Billington, S.J.; Huggins, A.S.; Johansen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, N
Infect. Immun. 67, 1277-1286, 1999
A;Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) c
A;Reference number: Z18734; MUID:99150261; PMID:10024571
A;Accession: TI7380
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-118 <BIL>
A;Cross-references: EMBL:U20246; NID:G3493323; PID:G3482862; PIDN:AAC33389.1
A;Experimental source: strtain A198

Query Match 7.0%; Score 6; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LEQVSG 35
|||||
Db 80 LEQVSG 85

RESULT 34
D82022
truncated pilin NMA0272 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: D82022
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: D82022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83580.1; PID:g737903
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: pilS8; NMA0272

Query Match 7.0%; Score 6; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 GNEIDT 53
|||||
Db 49 GNEIDT 54

RESULT 35
E89984
hypothetical protein SA1762 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: E89984
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E89984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-124 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701745; PIDN:BAB43038.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1762

Query Match 7.0%; Score 6; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 DENLEQ 32
|||||
Db 62 DENLEQ 67

RESULT 36
AH3491
hypothetical cytosolic protein BMEI1918 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AH3491
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3491
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53099.1; PID:g17983964; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1918
A:Map position: 1

Query Match 7.0%; Score 6; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 VSGILG 38
|||||
Db 112 VSGILG 117

RESULT 37
T46908
hypothetical protein DKFZp761G2423.1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 19-May-2000
C:Accession: T46908
R:Boecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24137
A:Accession: T46908
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-138 <AAA>
A:Cross-references: EMBL:AL136571
A:Experimental source: adult amygdala; clone DKFZp761G2423
C:Genetics:
A:Note: DKFZp761G2423.1
C:Superfamily: Saccharomyces probable membrane protein YMR292w

Query Match 7.0%; Score 6; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFIRRV 17
|||||
Db 107 GFIRRV 112

RESULT 38
T39245
ef-hand protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C:Accession: T39245
R:Wedler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21742
A:Accession: T39245
A:Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A:Residues: 1-141 <WED>
A:Cross-references: EMBL:AL117210; PIDN:CAB55175.1; GSPDB:GN00066; SPDB:SPAP8A3.08
A:Experimental source: strain 972h-; clone p1 p8A3
C:Genetics:
A:Gene: SPDB:SPAP8A3.08
A:Map position: 1
A:Introns: 11/1; 55/1; 102/1; 133/1

C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand

Query Match 7.0%; Score 6; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 NEEMDE 28
Db 112 NEEMDE 117

RESULT 39

C44259
kinesin heavy chain homolog KIF5 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
C;Accession: C44259
R;Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous system.
A;Reference number: A44259; MUID:93077686; PMID:1447303

A;Accession: C44259
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-143 <AIZ>

A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118906)
C;Superfamily: kinesin heavy chain; kinesin motor domain homology
F;1-143/Domain: kinesin motor domain homology (fragment) <XMOT>

Query Match 7.0%; Score 6; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 MDENLE 31
Db 35 MDENLE 40

RESULT 40

S31243
ribosomal protein Yml28 precursor, mitochondrial - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YDR462w

C;Species: Saccharomyces cerevisiae
C;Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 19-Apr-2002
C;Accession: S31243; S69630; S17269
R;Wang, S.S.; Stanford, D.R.; Silvers, C.D.; Hopper, A.K.
Mol. Cell. Biol. 12, 2633-2643, 1992

A;Title: STP1, a gene involved in pre-tRNA processing, encodes a nuclear protein containing

A;Reference number: S31243; MUID:92269836; PMID:1588961

A;Accession: S31243

A;Molecule type: DNA

A;Residues: 1-147 <WAN>

A;Cross-references: EMBL:M88597; NID:g172767; PIDN:AAA35123.1; PID:g172768

R;Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A;Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.

A;Reference number: S69554

A;Accession: S69630

A;Molecule type: DNA

A;Residues: 1-147 <DIE>

A;Cross-references: EMBL:U33050; NID:g927726; PID:g927728; MIPS:YDR462w

R;Grohmann, L.; Graack, H.R.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
FEBS Lett. 284, 51-56, 1991

A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from

A;Reference number: S17255; MUID:91285106; PMID:2060626

A;Accession: S17269

A;Molecule type: protein

A;Residues: 'XIF', 30-32, 'VI', 35, 'VI', 38-43, 'X', 45-46, 'X', 48, 'KX', 51-52, 'P' <GRO>

A;Experimental source: strain 07173

C;Genetics:

A;Gene: SGD:MRPL28; MRPL28

A;Cross-references: MIPS:YDR462w; SGD:S0002870

A;Map position: 4R

A;Genome: nuclear

C;Keywords: mitochondrion; protein biosynthesis; ribosome

F;1-26/Domain: transit peptide (mitochondrion) #status experimental <TNP>

F;27-147/Product: ribosomal protein Yml28 #status experimental <MAT>

Query Match 7.0%; Score 6; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LEQVSG 35
Db 14 LEQVSG 19

RESULT 41

G95210

acetyltransferase, GNAT family [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: G95210

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf, E.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: G95210

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-148 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75880.1; PID:g14973306; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SPI807

Query Match 7.0%; Score 6; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 EANQRA 79
Db 115 EANQRA 120

RESULT 42

A98075

conserved hypothetical protein spr1627 [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C;Accession: A98075

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; I

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: A98075

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-148 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAL00430.1; PID:g15459297; GSPDB:GN00174

C;Genetics:

A;Gene: spr1627

Query Match 7.0%; Score 6; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 EANQRA 79

Db 115 EANORA 120
|||||
RESULT 43
AC1608
arginine repressor homolog lin1404 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1608
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1608
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96635.1; PID:g16413877; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1404
C;Superfamily: Escherichia coli arginine repressor argR
Query Match 7.0%; Score 6; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 NEIDTQ 54
|||||
Db 17 NEIDTQ 22

RESULT 44
AG1245
arginine repressor homolog lmol367 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AG1245
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1245
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99445.1; PID:g16410783; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmol367
C;Superfamily: Escherichia coli arginine repressor argR
Query Match 7.0%; Score 6; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 NEIDTQ 54
|||||
Db 17 NEIDTQ 22

RESULT 45
A83053
conserved hypothetical protein PA4746 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83053
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83053
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <STO>
A;Cross-references: GB:AE004888; GB:AE004091; NID:9951001; PIDN:AAG08132.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4746
C;Superfamily: nus operon 15K protein
Query Match 7.0%; Score 6; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 QVSGIL 37
|||||
Db 58 QVSGIL 63

Search completed: March 4, 2004, 08:34:44
Job time : 22 secs

```

; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match          57.0%; Score 49; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
      |||||
Db 158 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
      |||||

RESULT 8
US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19

```

Fri Mar 5 07:11:12 2004

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```

OM protein - protein search, using sw model

Run on:      March  4, 2004, 08:32:56 ; Search time 34 Seconds
              (without alignments)
              534.094 Million cell updates/sec

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

```

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDREQMAISGGFIRRVTA.....SNKTRIDEANORATKWLGG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 809742 seqs, 211153259 residues

Word size : 0

Total number of hits satisfying chosen parameters: 809742

```
Minimum DB seq length: 0
Maximum DB seq length: 200000000
```

Post-processing: Listing first 45 summaries

```

Database : Published Applications AA:*
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

```

```

BEST LOCAL SIMILARITY 100.00%; FILED. NO. 1-106-121;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
      |||||
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 3
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match 57.0%; Score 49; DB 10; Length 206;
Best Local Similarity 100.00%;

```

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```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33

Query Match          38.4%; Score 33; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 8.3e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      54  QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
      ||||||||||||||||||||||||||||||||
Db      1  QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33

RESULT 12
US-09-942-098-38
; Sequence 38, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-38

Query Match          38.4%; Score 33; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 8.3e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      54  QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
      ||||||||||||||||||||||||||||||||
Db      1  QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33

```

RESULT 14
US-09-942-024-16
Classification: NO/NOQ42024

; FILE REFERENCE: P-AR 4802


```
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-90

Query Match      25.6%; Score 22; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      65 ADSNKTTRIDEANQRATKMLGSG 86
Db      2 ADSNKTTRIDEANQRATKMLGSG 23

RESULT 20
US-09-942-024-37
; Sequence 37, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-37

Query Match      25.6%; Score 22; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      65 ADSNKTTRIDEANQRATKMLGSG 86
Db      12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 21
US-09-942-098-37
; Sequence 37, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-37

Query Match      25.6%; Score 22; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      65 ADSNKTTRIDEANQRATKMLGSG 86
Db      12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 22
US-09-942-024-88
; Sequence 88, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-88

Query Match      24.4%; Score 21; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      66 DSNKTTRIDEANQRATKMLGSG 86
Db      2 DSNKTTRIDEANQRATKMLGSG 22

RESULT 23
US-09-942-098-88
; Sequence 88, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-88
```

```
Query Match      24.4%; Score 21; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      66 DSNKTRIDEANQRAKMLGSG 86
      |||||||
Db      2 DSNKTRIDEANQRAKMLGSG 22
```

```
RESULT 24
US-09-942-024-89
; Sequence 89, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-89
```

```
Query Match      22.1%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      65 ADSNKTRIDEANQRAKML 83
      |||||||
Db      2 ADSNKTRIDEANQRAKML 20
```

```
RESULT 25
US-09-942-098-89
; Sequence 89, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
```

```
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-89
```

```
Query Match      22.1%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      65 ADSNKTRIDEANQRAKML 83
      |||||||
Db      2 ADSNKTRIDEANQRAKML 20
```

```
RESULT 26
US-09-942-024-32
; Sequence 32, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-32
```

```
Query Match      20.9%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      66 DSNKTRIDEANQRAKML 83
      |||||||
Db      1 DSNKTRIDEANQRAKML 18
```

```
RESULT 27
US-09-942-098-32
; Sequence 32, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
```

; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-32

Query Match 20.9%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DSNKTRIDEANQRATKML 83
| | | | | | | | | | | | | | | | | |
Db 1 DSNKTRIDEANQRATKML 18

RESULT 28
US-09-942-024-93
; Sequence 93, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-93

Query Match 20.9%; Score 18; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 KTRIDEANQRATKMLGSG 86
| | | | | | | | | | | | | | | | | |
Db 4 KTRIDEANQRATKMLGSG 21

RESULT 29
US-09-942-098-93
; Sequence 93, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098

; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-93

Query Match 20.9%; Score 18; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 KTRIDEANQRATKMLGSG 86
| | | | | | | | | | | | | | | | | |
Db 4 KTRIDEANQRATKMLGSG 21

RESULT 30
US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-30

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRATKML 83
| | | | | | | | | | | | | | | | | |
Db 1 SNKTRIDEANQRATKML 17

RESULT 31
US-09-942-024-31
; Sequence 31, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-31

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DSNKTRIDEANQRTKML 82
| | | | | | | | | | | | | | | | | | | | |
Db 1 DSNKTRIDEANQRTKML 17

RESULT 32
US-09-942-098-30
; Sequence 30, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-30

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRTKML 83
| | | | | | | | | | | | | | | | | | | | |
Db 1 SNKTRIDEANQRTKML 17

RESULT 33
US-09-942-098-31
; Sequence 31, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-31

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DSNKTRIDEANQRTKML 82
| | | | | | | | | | | | | | | | | | | | |

Db 1 DSNKTRIDEANQRTKML 17

RESULT 34
US-10-011-588-2
; Sequence 2, Application US/10011588
; Publication No. US20020168727A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Leonard
; APPLICANT: Jensen, Melody
; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
; FILE REFERENCE: A34796 067252.0113
; CURRENT APPLICATION NUMBER: US/10/011,588
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/910,186
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/246,744
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 60/311,966
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2

Query Match 19.8%; Score 17; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRTKML 83
| | | | | | | | | | | | | | | | | | | | |
Db 1 SNKTRIDEANQRTKML 17

RESULT 35
US-09-942-024-92
; Sequence 92, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION

```
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-92
```

```
Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      70 TRIDEANQRATKMLGSG 86
      |||||||
Db      2 TRIDEANQRATKMLGSG 18
```

```
RESULT 36
US-09-942-024-95
; Sequence 95, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=DABCYL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=EDANS modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-95
```

```
Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      70 TRIDEANQRATKMLGSG 86
      |||||||
Db      2 TRIDEANQRATKMLGSG 18
```

```
RESULT 37
US-09-942-098-92
; Sequence 92, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-92
```

```
Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      70 TRIDEANQRATKMLGSG 86
      |||||||
Db      2 TRIDEANQRATKMLGSG 18
```

```
RESULT 38
US-09-942-098-95
; Sequence 95, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=DABCYL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=EDANS modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-95
```

```
Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      70 TRIDEANQRATKMLGSG 86
      |||||||
Db      2 TRIDEANQRATKMLGSG 18
```

```
RESULT 39
US-09-942-024-29
; Sequence 29, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
```


; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-29

Query Match 18.6%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANQRATKM 82
Db 1 SNKTRIDEANQRATKM 16
|||||

RESULT 40
US-09-942-098-29
; Sequence 29, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-29

Query Match 18.6%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANQRATKM 82
Db 1 SNKTRIDEANQRATKM 16
|||||

RESULT 41
US-09-942-024-85
; Sequence 85, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 1

; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 20
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-85

Query Match 18.6%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 NKTRIDEANQRATKML 83
Db 3 NKTRIDEANQRATKML 18
|||||

RESULT 42
US-09-942-098-85
; Sequence 85, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 20
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-85

Query Match 18.6%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 NKTRIDEANQRATKML 83
Db 3 NKTRIDEANQRATKML 18
|||||

RESULT 43
US-09-942-024-28
; Sequence 28, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-28

Query Match 17.4%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANQRATK 81
Db 1 SNKTRIDEANQRATK 15

RESULT 44

US-09-942-098-28
; Sequence 28, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-28

Query Match 17.4%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANQRATK 81
Db 1 SNKTRIDEANQRATK 15

RESULT 45

US-09-942-024-44
; Sequence 44, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-942-024-44

Query Match 17.4%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANQRATK 81
Db 1 SNKTRIDEANQRATK 15

Search completed: March 4, 2004, 08:36:05
Job time : 34 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:31:50 ; Search time 22 Seconds
(without alignments)
201.811 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDEREQMAISGGFIRRVVNA.....SNKTRIDEANQRATKMLGSG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 389414 seqs, 51625971 residues

Word size : 0
Total number of hits satisfying chosen parameters: 389414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	49	57.0	70	2	US-08-760-001-10
2	49	57.0	70	3	US-09-015-960-10
3	49	57.0	70	4	US-09-534-572-10
4	49	57.0	206	1	US-08-393-985-18
5	49	57.0	206	3	US-08-819-286-1
6	37	43.0	37	3	US-08-819-286-4
7	26	30.2	26	3	US-08-819-286-8
8	20	23.3	20	3	US-08-819-286-7
9	20	23.3	20	3	US-08-819-286-9
10	17	19.8	17	2	US-08-743-894B-1
11	17	19.8	17	2	US-08-743-894B-37
12	16	18.6	16	2	US-08-743-894B-49
13	16	18.6	16	3	US-08-819-286-12
14	15	17.4	15	2	US-08-743-894B-38
15	15	17.4	17	2	US-08-743-894B-24
16	15	17.4	17	2	US-08-743-894B-28
17	14	16.3	17	2	US-08-743-894B-31
18	13	15.1	13	4	US-09-976-535A-1
19	13	15.1	17	2	US-08-743-894B-19
20	13	15.1	17	2	US-08-743-894B-25
21	13	15.1	17	2	US-08-743-894B-26
22	13	15.1	17	2	US-08-743-894B-32
23	12	14.0	12	2	US-08-743-894B-41
24	12	14.0	13	3	US-08-750-101-11
25	12	14.0	14	4	US-09-976-535A-2
26	12	14.0	17	2	US-08-743-894B-27
27	12	14.0	17	2	US-08-743-894B-36

28	12	14.0	17	2	US-08-743-894B-39	Sequence 39, Appl
29	12	14.0	17	2	US-08-743-894B-42	Sequence 42, Appl
30	11	12.8	13	2	US-08-743-894B-16	Sequence 16, Appl
31	11	12.8	13	4	US-09-976-535A-13	Sequence 13, Appl
32	11	12.8	16	2	US-08-743-894B-51	Sequence 51, Appl
33	11	12.8	16	2	US-08-743-894B-52	Sequence 52, Appl
34	11	12.8	16	2	US-08-743-894B-54	Sequence 54, Appl
35	11	12.8	17	2	US-08-743-894B-2	Sequence 2, Appl
36	11	12.8	17	2	US-08-743-894B-6	Sequence 6, Appl
37	11	12.8	17	2	US-08-743-894B-43	Sequence 43, Appl
38	11	12.8	17	2	US-08-743-894B-44	Sequence 44, Appl
39	11	12.8	17	2	US-08-743-894B-45	Sequence 45, Appl
40	11	12.8	17	2	US-08-743-894B-47	Sequence 47, Appl
41	10	11.6	12	2	US-08-743-894B-17	Sequence 17, Appl
42	10	11.6	13	4	US-09-976-535A-11	Sequence 11, Appl
43	10	11.6	13	4	US-09-976-535A-12	Sequence 12, Appl
44	10	11.6	14	4	US-09-976-535A-6	Sequence 6, Appl
45	10	11.6	16	2	US-08-743-894B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-760-001-10

Query Match 57.0%; Score 49; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATKMLGSG 86
Db 22 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATKMLGSG 70

RESULT 2

US-09-015-960-10
; Sequence 10, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-015-960-10

Query Match 57.0%; Score 49; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATKMLGSG 86
Db 22 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATKMLGSG 70

RESULT 3

US-09-534-572-10
; Sequence 10, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-534-572-10

Query Match 57.0%; Score 49; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATKMLGSG 86
Db 22 GNLRHVMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATKMLGSG 70

RESULT 4

US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-393-985-18

Query Match 57.0%; Score 49; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 86
Db 158 GNLHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 206

RESULT 5
US-08-819-286-1
Sequence 1, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-1

Query Match 57.0%; Score 49; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 86
Db 158 GNLHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 206

Db 158 GNLHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 206

RESULT 6
US-08-819-286-4
Sequence 4, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-4

Query Match 43.0%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 EIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 86
Db 1 EIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 37

RESULT 7
US-08-819-286-8
Sequence 8, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037


```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-8

```

```

Query Match 30.2%; Score 26; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.7e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 IMEKADSNKTRIDEANQKATKMLGSG 86
Db 1 IMEKADSNKTRIDEANQKATKMLGSG 26

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```

RESULT 8
US-08-819-286-7
; Sequence 7, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-7

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```

Query Match 23.3%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 50 EIDTONRQIDRIMEKADSNK 69
Db 1 EIDTONRQIDRIMEKADSNK 20

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RESULT 9
US-08-819-286-9
; Sequence 9, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-9

```

```

Query Match 23.3%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 67 SNKTRIDEANQKATKMLGSG 86
Db 1 SNKTRIDEANQKATKMLGSG 20

```

```

RESULT 10
US-08-743-894B-1
; Sequence 1, Application US/08743894B

```

Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MPMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-743-894B-1
Query Match 19.8%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 SNKTRIDEANQRATKML 83
Db 1 SNKTRIDEANQRATKML 17
RESULT 11
US-08-743-894B-37
Sequence 37, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MPMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-37
Query Match 19.8%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 SNKTRIDEANQRATKML 83
Db 1 SNKTRIDEANQRATKML 17
RESULT 12
US-08-743-894B-49
Sequence 49, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MPMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-49

Query Match 18.6%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRATKM 82
|||||
Db 1 SNKTRIDEANQRATKM 16

RESULT 13
US-08-819-286-12
; Sequence 12, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-12

Query Match 18.6%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QNRQIDRIMEKADSNK 69
|||||
Db 1 QNRQIDRIMEKADSNK 16

RESULT 14
US-08-743-894B-38
; Sequence 38, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty

; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699member 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
US-08-743-894B-38

Query Match 17.4%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRATK 81
|||||
Db 1 SNKTRIDEANQRATK 15

RESULT 15
US-08-743-894B-24
; Sequence 24, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699member 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
LOCATION: 16
OTHER INFORMATION: Xaa represents norleucine
US-08-743-894B-24

Query Match 17.4%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRA TK 81
Db 1 SNKTRIDEANQRA TK 15

RESULT 16
US-08-743-894B-28
; Sequence 28, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MRC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
US-08-743-894B-28

Query Match 17.4%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRA TK 81

Db 1 SNKTRIDEANQRA TK 15

RESULT 17
US-08-743-894B-31
; Sequence 31, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MRC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
US-08-743-894B-31

Query Match 16.3%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRA TK 80
Db 1 SNKTRIDEANQRA TK 14

RESULT 18
US-09-976-535A-1
; Sequence 1, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

```
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human
US-09-976-535A-1

Query Match      15.1%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      70 TRIDEANQRATKM 82
Db      1 TRIDEANQRATKM 13

RESULT 19
US-08-743-894B-19
; Sequence 19, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 4
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-19

Query Match      15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      71 RIDEANQRATKML 83
Db      5 RIDEANQRATKML 17

RESULT 20
US-08-743-894B-25
; Sequence 25, Application US/08743894B
; Patent No. 5965699
```

```
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 14
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
US-08-743-894B-25

Query Match      15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 SNKTRIDEANQRA 79
Db      1 SNKTRIDEANQRA 13

RESULT 21
US-08-743-894B-26
; Sequence 26, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
```


APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-26

Query Match 15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRA 79
|||||
Db 1 SNKTRIDEANQRA 13

RESULT 22

US-08-743-894B-32
Sequence 32, Application US/08743894B
Patent No. 5965699

GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MPMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:

US-08-743-894B-32

Query Match 15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRA 79
|||||
Db 1 SNKTRIDEANQRA 13

RESULT 23

US-08-743-894B-41
Sequence 41, Application US/08743894B
Patent No. 5965699

GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MPMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:

US-08-743-894B-41

Query Match 14.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IDEANQRAKML 83
|||||
Db 1 IDEANQRAKML 12

RESULT 24

US-08-750-101-11
Sequence 11, Application US/08750101B
Patent No. 6203794

GENERAL INFORMATION:
APPLICANT: Dolly, James Oliver
APPLICANT: Aoki, Roger Kei
APPLICANT: Wheeler, Larry
APPLICANT: Elwood, Micheal

;
; TITLE OF INVENTION: MODIFICATION OF CLOSTRIDIAL TOXINS FOR
; TITLE OF INVENTION: USE AS TRANSPORT PROTEINS
; FILE REFERENCE: 17044
; CURRENT APPLICATION NUMBER: US/08/750,101B
; CURRENT FILING DATE: 1997-05-01
; EARLIER APPLICATION NUMBER: PCT/GB/01253
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: UK 9410871.9
; EARLIER FILING DATE: 1994-05-31
; EARLIER APPLICATION NUMBER: UK 9410871.1
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Portion of predicted amino acid sequence of human
; OTHER INFORMATION: SNAP-25.
US-08-750-101-11

Query Match 14.0%; Score 12; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 ANQRATKMLGSG 86
|||||
Db 2 ANQRATKMLGSG 13

RESULT 25

US-09-976-535A-2
; Sequence 2, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc.feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
; NAME/KEY: misc.feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa represents D-Lys
US-09-976-535A-2

Query Match 14.0%; Score 12; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 TRIDEANQRATK 81
|||||
Db 1 TRIDEANQRATK 12

RESULT 26

US-08-743-894B-27
; Sequence 27, Application US/08743894B
; Patent No. 5965699

;
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-27

Query Match 14.0%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANQR 78
|||||
Db 1 SNKTRIDEANQR 12

RESULT 27

US-08-743-894B-36
; Sequence 36, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-36

Query Match 14.0%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IDEANQRATKML 83
Db 6 IDEANQRATKML 17

RESULT 28
US-08-743-894B-39
; Sequence 39, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:

Query Match 14.0%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IDEANQRATKML 83
Db 6 IDEANQRATKML 17

US-08-743-894B-39

Query Match 14.0%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQR 78
Db 1 SNKTRIDEANQR 12

RESULT 29
US-08-743-894B-42
; Sequence 42, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
US-08-743-894B-42

Query Match 14.0%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQR 78
Db 1 SNKTRIDEANQR 12

RESULT 30
US-08-743-894B-16
; Sequence 16, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
;; STREET: USA MPMC - 504 Scott Street
;; CITY: FORT DETRICK
;; STATE: MARYLAND
;; COUNTRY: USA
;; ZIP: 21702-5012

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.0
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,894B
;; FILING DATE: No. 5965699ember 6, 1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Charles H. Harris
;; REGISTRATION NUMBER: 34,616
;; REFERENCE/DOCKET NUMBER:
;; TELEPHONE: (301) 619-2065
;; TELEFAX: (301) 619-7714
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid sequence
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; FEATURE:

US-08-743-894B-16

Query Match 12.8%; Score 11; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORAT 80
|||||
DB 1 TRIDEANORAT 11

RESULT 31

US-09-976-535A-13
; Sequence 13, Application US/09976535A
; Patent No. 6504006

;; GENERAL INFORMATION:
;; APPLICANT: Shine, Nancy R.
;; APPLICANT: Crawford, Karen R.
;; APPLICANT: Eaton, Linda J.
;; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
;; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
;; FILE REFERENCE: P010018
;; CURRENT APPLICATION NUMBER: US/09/976,535A
;; CURRENT FILING DATE: 2001-10-12
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 13
;; LENGTH: 13

;; TYPE: PRT
;; ORGANISM: artificial sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
;; NAME/KEY: misc feature
;; LOCATION: (2)..(2)
;; OTHER INFORMATION: Xaa represents D-Arg

US-09-976-535A-13

Query Match 12.8%; Score 11; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IDEANORATKM 82
|||||
DB 3 IDEANORATKM 13

RESULT 32

US-08-743-894B-51
; Sequence 51, Application US/08743894B
; Patent No. 5965699

;; GENERAL INFORMATION:
;; APPLICANT: James J. Schmidt
;; APPLICANT: Karen A. Bostian
;; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
;; STREET: USA MPMC - 504 Scott Street
;; CITY: FORT DETRICK
;; STATE: MARYLAND
;; COUNTRY: USA
;; ZIP: 21702-5012

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.0
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,894B
;; FILING DATE: No. 5965699ember 6, 1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Charles H. Harris
;; REGISTRATION NUMBER: 34,616
;; REFERENCE/DOCKET NUMBER:
;; TELEPHONE: (301) 619-2065
;; TELEFAX: (301) 619-7714
;; INFORMATION FOR SEQ ID NO: 51:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid sequence
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; FEATURE:

US-08-743-894B-51

Query Match 12.8%; Score 11; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORAT 80
|||||
DB 4 TRIDEANORAT 14

RESULT 33

US-08-743-894B-52
; Sequence 52, Application US/08743894B
; Patent No. 5965699

;; GENERAL INFORMATION:
;; APPLICANT: James J. Schmidt
;; APPLICANT: Karen A. Bostian
;; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
;; STREET: USA MPMC - 504 Scott Street
;; CITY: FORT DETRICK
;; STATE: MARYLAND

COUNTRY: USA
 ZIP: 21702-5012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.0
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/743,894B
 FILING DATE: No. 5965699ember 6, 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Charles H. Harris
 REGISTRATION NUMBER: 34,616
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid sequence
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 FEATURE:
 LOCATION: 16
 OTHER INFORMATION: Xaa represents Nle, or No. 5965699leucine
 US-08-743-894B-52

Query Match 12.8%; Score 11; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANQRAT 80
 |||||
 Db 4 TRIDEANQRAT 14

RESULT 34
 US-08-743-894B-54
 ; Sequence 54, Application US/08743894B
 ; Patent No. 5965699
 ; GENERAL INFORMATION:
 ; APPLICANT: James J. Schmidt
 ; APPLICANT: Karen A. Bostian
 ; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
 ; STREET: USA MRM - 504 Scott Street
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.0
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/743,894B
 ; FILING DATE: No. 5965699ember 6, 1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid sequence
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 FEATURE:
 LOCATION: 16
 OTHER INFORMATION: Xaa represents Nle, or No. 5965699leucine
 US-08-743-894B-54

Query Match 12.8%; Score 11; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANQRAT 80
 |||||
 Db 4 TRIDEANQRAT 14

RESULT 35
 US-08-743-894B-2
 ; Sequence 2, Application US/08743894B
 ; Patent No. 5965699
 ; GENERAL INFORMATION:
 ; APPLICANT: James J. Schmidt
 ; APPLICANT: Karen A. Bostian
 ; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
 ; STREET: USA MRM - 504 Scott Street
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.0
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/743,894B
 ; FILING DATE: No. 5965699ember 6, 1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid sequence
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-743-894B-2

Query Match 12.8%; Score 11; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANQRAT 80
 |||||
 Db 4 TRIDEANQRAT 14

```

RESULT 36
US-08-743-894B-6
; Sequence 6, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 43:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-43
; Query Match 12.8%; Score 11; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 7.8e-05;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANQRAT 80
Db 4 TRIDEANQRAT 14

RESULT 37
US-08-743-894B-43
; Sequence 43, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 16
; OTHER INFORMATION: Xaa represent Mle, or No. 5965699eleucine
; US-08-743-894B-6
; Query Match 12.8%; Score 11; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 7.8e-05;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANQRAT 80
Db 4 TRIDEANQRAT 14

RESULT 38
US-08-743-894B-44
; Sequence 44, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7714
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 11:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-44
; Query Match 12.8%; Score 11; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 7.8e-05;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQ 77
Db 1 SNKTRIDEANQ 11

```



```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 12
; OTHER INFORMATION: Xaa represents 2-aminopentanoic acid or norvaline
US-08-743-894B-44
    Query Match      12.8%; Score 11; DB 2; Length 17;
    Best Local Similarity 100.0%; Pred. No. 7.8e-05;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      67 SNKTRIDEANQ 77
Db      1 SNKTRIDEANQ 11

RESULT 39
US-08-743-894B-45
; Sequence 45, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-45
    Query Match      12.8%; Score 11; DB 2; Length 17;
    Best Local Similarity 100.0%; Pred. No. 7.8e-05;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      67 SNKTRIDEANQ 77
Db      1 SNKTRIDEANQ 11

RESULT 40
```

```
US-08-743-894B-47
; Sequence 47, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-47
    Query Match      12.8%; Score 11; DB 2; Length 17;
    Best Local Similarity 100.0%; Pred. No. 7.8e-05;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      67 SNKTRIDEANQ 77
Db      1 SNKTRIDEANQ 11

RESULT 41
US-08-743-894B-17
; Sequence 17, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MPMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
;
US-08-743-894B-17
    Query Match      12.8%; Score 11; DB 2; Length 17;
    Best Local Similarity 100.0%; Pred. No. 7.8e-05;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      67 SNKTRIDEANQ 77
Db      1 SNKTRIDEANQ 11
```

RESULT 43

RESULT 45
US-08-743-894B-7
; Sequence 7, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 4
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-7

Query Match 11.6%; Score 10; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQRAT 80
|||
Db 5 RIDEANQRAT 14

Search completed: March 4, 2004, 08:35:18
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:27:55 ; Search time 54 Seconds
(without alignments)
449.983 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDREQMAISGGFIRRTNA.....SNKTRIDEANQRATKMLGSG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	86	100.0	86	AAB15584	Human SNA
2	49	57.0	70	AAR86823	SNAP-25 r
3	49	57.0	116	AAO15165	Clostridi
4	49	57.0	206	AAW30103	Synapto
5	49	57.0	206	AAW43426	Mouse syn
6	49	57.0	206	AAW79198	Mouse SNA
7	49	57.0	206	AAU00246	Synapto
8	49	57.0	206	AAU00253	SNARE hom
9	49	57.0	206	AAU00252	SNARE hom
10	49	57.0	206	AAE36662	Human SNA
11	49	57.0	206	AAE36667	Rat VAMP-
12	49	57.0	206	ADE54280	Rat Prote
13	49	57.0	206	ADE54288	Rat Prote
14	49	57.0	206	ADE54276	Rat Prote
15	49	57.0	206	ADE54290	Human Pro
16	49	57.0	206	ADE54282	Rat Prote
17	49	57.0	206	ADE54274	Rat Prote
18	49	57.0	206	ADE54286	Human Pro
19	49	57.0	206	ADE54284	Rat Prote
20	49	57.0	206	ADE54272	Rat Prote
21	49	57.0	206	ADE54278	Rat Prote
22	45	52.3	206	AAU02640	Synapto
23	44	51.2	206	AAU02638	Synapto
24	41	47.7	198	AAU00255	Synapto
25	40	46.5	116	AAO15166	Clostridi

26	40	46.5	199	4	AAU00263	Synapto
27	40	46.5	200	4	AAU00264	Synapto
28	40	46.5	201	4	AAU02637	Synapto
29	40	46.5	202	4	AAU00265	Synapto
30	40	46.5	203	4	AAU02636	Synapto
31	40	46.5	206	4	AAU00261	Synapto
32	40	46.5	206	4	AAU02171	Synapto
33	40	46.5	206	4	AAU00259	Synapto
34	40	46.5	206	4	AAU02639	Synapto
35	39	45.3	206	4	AAU00256	Synapto
36	39	45.3	206	4	AAU00266	Synapto
37	39	45.3	206	4	AAU00258	Synapto
38	39	45.3	206	4	AAU00262	Synapto
39	39	45.3	206	4	AAU00260	Synapto
40	39	45.3	206	4	AAU00257	Synapto
41	37	43.0	37	2	AAW30097	Neurotran
42	33	38.4	33	6	AAE36683	Goldfish
43	33	38.4	33	6	AAE36678	SNAP-25 p
44	27	31.4	49	4	AAM57386	Human bra
45	26	30.2	26	2	AAW30099	Neurotran

ALIGNMENTS

RESULT 1
AAB15584
ID AAB15584 standard; peptide; 86 AA.
XX
AC AAB15584;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human SNAP-25 N-terminal peptide #4.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptoosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN WO200064932-A1.
XX
PD 02-NOV-2000.
XX
PF 18-FEB-2000; 2000WO-ES000058.
XX
PR 23-APR-1999; 99ES-00000844.
XX
XX (LIPO-) LIPOTEC SA.
XX
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez IM, Carbonell Castell T;
PI Perez Paya E;
XX
WPI; 2001-007091/01.
XX
PT New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders.
XX
PS Claim 16; Page 32-33; 40pp; Spanish.
XX
CC The invention relates to new peptides comprising 3-30 contiguous amino
CC acids from the N-terminus of the protein SNAP-25 (synaptoosomal-associated
CC protein 25). The peptides AAB15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
CC neurodegenerative disorders
XX
SQ Sequence 86 AA;

```
Query Match      100.0%; Score 86; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDREQMAISGGFIRRVTNARENEEMDENLEQVSGILGNLRHMDMGNEIDTQNRQIDR 60
   |||||
Db 1 VDREQMAISGGFIRRVTNARENEEMDENLEQVSGILGNLRHMDMGNEIDTQNRQIDR 60
   |||||

QY 61 IMEKADSNKTRIDEANQRATKMLGSG 86
   |||||
Db 61 IMEKADSNKTRIDEANQRATKMLGSG 86

RESULT 2
AAR86823
ID AAR86823 standard; peptide; 70 AA.
XX
AC AAR86823;
XX
DT 15-AUG-1996 (first entry)
XX
DE SNAP-25 residues 137-206.
XX
KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;
KW antibody; detection; assay.
XX
OS Synthetic.
XX
PN WO9533850-A1.
XX
PD 14-DEC-1995.
XX
PF 02-JUN-1995; 95WO-GB001279.
XX
PR 03-JUN-1994; 94GB-0001138.
XX
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
PI Shone CC, Hallis B, James BAF, Quinn CP;
XX
DR WPI; 1996-040249/04.
XX
PT Assay for botulinum or tetanus toxin - by combining test cpd. with
PT substrate which is cleaved by the toxin, and antibody specific for the
PT cleaved but not uncleaved substrate.
XX
PS Example 4; Page 19; 48pp; English.
XX
CC The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. Assays for botulinum types A
CC and E use the present sequence as a substrate. The sequence is SNAP-25
CC protein, residues 137-206
XX
SQ Sequence 70 AA;

Query Match      57.0%; Score 49; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.1e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
   |||||
Db 22 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 70
   |||||

RESULT 3
AAO15165
ID AAO15165 standard; peptide; 116 AA.

Query Match      57.0%; Score 49; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
   |||||
Db 67 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 115
   |||||

RESULT 4
AAW30103
ID AAW30103 standard; peptide; 206 AA.
XX
AC AAW30103;
XX
DT 06-APR-1998 (first entry)
XX
```

```
XX
AC AAO15165;
XX
DT 02-SEP-2002 (first entry)
XX
DE Clostridial neurotoxin protease substrate peptide 4.
XX
KW Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
KW fluorescence resonant energy transfer assay; quenched-signal;
KW clostridial neurotoxin detection; food.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "S-fluoresceinyl-cysteine"
FT Cleavage-site 89..90
FT /note= "The peptide is cleaved between these two residues
FT by type E Clostridium botulinum neurotoxin"
FT Cleavage-site 106..107
FT /note= "The peptide is cleaved between these two residues
FT by type A Clostridium botulinum neurotoxin"
XX
PN WO200225284-A2.
XX
PD 28-MAR-2002.
XX
PF 25-SEP-2001; 2001WO-US030188.
XX
PR 25-SEP-2000; 2000US-0235050P.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Schmidt JJ, Stafford RG;
XX
DR WPI; 2002-499829/53.
XX
PT Substrate useful in e.g. an assay for the protease activity of
PT clostridial neurotoxin, comprises modified peptide or protein.
XX
PS Claim 22; Page 16; 48pp; English.
XX
CC The invention comprises clostridial neurotoxin substrate peptides which
CC can serve as fluorescence resonant energy transfer assay (FRET) or
CC quenched-signal substrates in assays for the proteolytic activities of
CC clostridial neurotoxins. The invention further comprises Clostridium
CC botulinum neurotoxin substrate peptides that can serve as immobilised
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
CC activities of clostridial neurotoxins. The clostridial (including the
CC Clostridium botulinum) neurotoxin substrate peptides are useful for
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
CC or an environmental sample). The present amino acid sequence represents a
CC clostridial neurotoxin substrate peptide of the invention
XX
SQ Sequence 116 AA;

Query Match      57.0%; Score 49; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
   |||||
Db 67 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 115
   |||||

RESULT 4
AAW30103
ID AAW30103 standard; peptide; 206 AA.
XX
AC AAW30103;
XX
DT 06-APR-1998 (first entry)
XX
```

DE Synaptosomal associated protein.
 XX
 KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX
 OS Homo sapiens.
 XX
 PN WO9734620-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US004393.
 XX
 PR 18-MAR-1996; 96US-0013599P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Montal M;
 XX
 DR WPI; 1997-479986/44.
 XX
 XX Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neuro:transmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 XX
 PS Disclosure; Page 27-28; 6lpp; English.
 XX
 CC This sequence represents the human 25 kD synaptosomal associated protein
 CC (SNAP-25), which is an inhibitory agent of the invention. The agents of
 CC the invention inhibit secretion of neurotransmitter from neuronal cells
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20
 CC amino acids (aa) all of which correspond substantially to any one of
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
 CC catecholamine secretion from bovine chromaffin cells at a concentration
 CC of 10 microm, especially 0.25 microm, or less. (I) are used, as a
 CC replacement for Clostridium toxin, to inhibit release of
 CC neurotransmitters from synaptic vesicles, specifically for reducing
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
 CC intracellular distribution of (I). Compounds for delivering the drug to
 CC neural cells provide targeted drug delivery, e.g. of substance P to brain
 CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
 CC toxic or immunogenic and are more readily available. Their therapeutic
 CC effect lasts for several days or weeks, so lower doses or less frequent
 CC treatments are required
 XX
 SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 5
 AAW43426
 ID AAW43426 standard; protein; 206 AA.
 XX
 AC AAW43426;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Mouse synaptosomal-associated protein-25.
 XX
 KW Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;
 KW neurotransmitter; presynaptic membrane; central nervous system; tumour;
 KW neurodegenerative disease; hormonal disorder; immunological disorder.
 XX
 OS Mus sp.

XX US5693476-A.
 PN
 XX
 PD 02-DEC-1997.
 XX
 PF 24-FEB-1995; 95US-00393985.
 XX
 PR 24-FEB-1995; 95US-00393985.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Scheller RH;
 XX
 DR WPI; 1998-031743/03.
 DR N-PSDB; AAV01554.
 XX
 PT Screening assay for modulators of syntaxin binding - using peptide
 PT comprising binding site of syntaxin, for identifying drugs useful for
 PT treating CNS disorders, neuro-degenerative diseases, etc.
 XX
 PS Disclosure; Col 67-72; 57pp; English.
 XX
 CC This amino acid sequence represents the mouse synaptosomal-associated
 CC protein of 25 kD (SNAP-25). The invention relates to a method for
 CC identifying a compound capable of affecting the binding of a syntaxin-
 CC binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to
 CC syntaxin. The method comprises measuring the effect of the test compound
 CC on the extent of binding between the SBP and the SBP-binding site on
 CC syntaxin. The method can be used for identifying drugs capable of
 CC inhibiting or stimulating neurotransmitter release at the active zones of
 CC presynaptic membranes, which may be useful for treating CNS disorders,
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or
 CC immunological disorders or tumours
 XX
 SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 6
 AAW79198
 ID AAW79198 standard; protein; 206 AA.
 XX
 AC AAW79198;
 XX
 DT 25-NOV-1998 (first entry)
 XX
 DE Mouse SNAP-25 polypeptide.
 XX
 KW Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking;
 KW calcium-regulated secretion; secretory vesicle; secretory process; brain;
 KW neurotransmitter release; presynaptic membrane; CNS disorder; depression;
 KW Parkinson's disease; endocrine system; hormonal imbalance; cell division;
 KW thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;
 KW immune system; antigen processing; immunomodulator; viral processing;
 KW central nervous system; vesicular release; affective disorder; human;
 KW anti-tumour application; membrane trafficking regulation; mouse.
 XX
 OS Mus sp.
 XX
 PN WO9838210-A2.
 XX
 PD 03-SEP-1998.
 XX
 PF 26-FEB-1998; 98WO-US003789.
 XX
 PR 26-FEB-1997; 97US-0039159P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX Bean AJ, Scheller RH;
 PI WPI; 1998-481140/41.
 XX N-PSDB; AAV57558.
 DR
 DR
 XX New isolated Hrs-2 nucleotidase - used in assays to identify compounds
 PT capable of modulating calcium-regulatory secretion of secretory vesicles,
 PT such as in neurotransmitter release.
 PT
 XX Claim 16; Page 42-44; 55pp; English.
 PS
 XX This represents a mouse SNAP-25 polypeptide, a component of the protein
 CC polypeptides thought to underlie vesicle docking and fusion. The
 CC invention provides rat and human Hrs-2 polypeptides which are ATP-
 CC preferring nucleotidase that associate with SNAP-25. For identifying a
 CC compound capable of modulating calcium-regulated secretion of secretory
 CC vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2
 CC polypeptide, in the presence and absence of a test compound. The effect
 CC of the test compound on the extent of binding between the SNAP-25 and Hrs
 CC -2 polypeptides are measured and a compound is identified as effective if
 CC its measured effect on the extent of binding is above a threshold level.
 CC The products can be used for identifying drugs capable of affecting
 CC secretory processes, such as neurotransmitter release at the active zones
 CC of presynaptic membranes. Such drugs can be used for treating disorders
 CC or conditions of the central nervous system by selectively enhancing or
 CC inhibiting vesicular release in specific areas of the brain, including
 CC affective disorders (e.g. depression), disorders of thought (e.g.
 CC schizophrenia) and degenerative disorders (Parkinson's disease), as well
 CC as applications such as anaesthesia. The drugs can also be used
 CC therapeutically in other systems such as the endocrine system for
 CC treatment of hormonal imbalances, the immune system for intervention in
 CC antigen processing, secreted immunomodulators, and viral processing, as
 CC well as anti-tumour applications, such as regulation of membrane
 CC trafficking during rapid cell division
 XX
 SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 7
 AAU00246
 ID AAU00246 standard; protein; 206 AA.
 XX AAU00246;
 AC
 XX 12-SEP-2001 (first entry)
 DT
 XX Synaptosomal-associated protein, SNAP25.
 DE
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mutagenic; PCR primer; mouse;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 180..181
 FT /note= "Peptide bond susceptible to cleavage by
 FT clostridial neurotoxin"
 FT Cleavage-site 197..198
 FT /note= "Peptide bonds susceptible to cleavage by

FT clostridial neurotoxin"
 XX WO200118038-A2.
 PN 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 PF 20-AUG-1999; 99US-0149993P.
 PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI WPI; 2001-226739/23.
 XX
 DR Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 PT
 XX Disclosure; Fig 8; 131pp; English.
 PS
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25. The sequence was used to create SNAP-25
 CC double/single point mutants and C-terminal deletion mutants used in a new
 CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)- attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE- dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state
 XX
 SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 8
 AAU00253.
 ID AAU00253 standard; protein; 206 AA.
 XX AAU00253;
 AC
 XX 12-SEP-2001 (first entry)
 DT
 XX SNARE homologue, synaptosomal-associated protein, hSNAP25b.
 DE
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; hSNAP25b; human.
 XX
 OS Homo sapiens.

XX WO200118038-A2.
 PN 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 PD 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI WPI; 2001-226739/23.
 DR N-PSDB; AAS00370.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Disclosure; Fig 8; 131pp; English.
 XX The sequence represents the amino acid sequence of SNARE homologue,
 CC synaptosomal-associated membrane protein, hSNAP25b, used during analysis
 CC of SNAP-25. SNAP-25 mutants were used in a new method of treating a
 CC patient suffering from poisoning or at risk of poisoning by a clostridial
 CC toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive
 CC fusion protein)-attachment protein receptor) to a cell of the patient,
 CC where the SNARE is resistant to proteolysis by the toxin (toxin-resistant
 CC SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory
 CC SNARE). The protein can be used in a method of treating a patient in need
 CC of inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis, comprises supplying a fragment,
 CC variant, fusion or derivative of a SNARE or an inhibitory SNARE to the
 CC cell of the patient. The toxin resistant or toxin inhibitory SNARE or a
 CC recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state
 XX Sequence 206 AA;
 SQ
 Query Match 57.0%; Score 49; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 9
 AAU00252
 ID AAU00252 standard; protein; 206 AA.
 XX AAU00252;
 AC AAU00252;
 XX 12-SEP-2001 (first entry)
 DT SNARE homologue, synaptosomal-associated protein, hSNAP25a.
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; hSNAP25a; human;
 KW N-ethylmaleimide-sensitive fusion;
 KW soluble NSF-attachment protein receptor.

XX Homo sapiens.
 OS WO200118038-A2.
 PN 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 PD 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI WPI; 2001-226739/23.
 DR N-PSDB; AAS00369.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Disclosure; Fig 8; 131pp; English.
 XX The sequence represents the amino acid sequence of SNARE homologue,
 CC synaptosomal-associated membrane protein, hSNAP25a, used during analysis
 CC of SNAP-25. SNAP-25 mutants were used in a new method of treating a
 CC patient suffering from poisoning or at risk of poisoning by a clostridial
 CC toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive
 CC fusion protein)-attachment protein receptor) to a cell of the patient,
 CC where the SNARE is resistant to proteolysis by the toxin (toxin-resistant
 CC SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory
 CC SNARE). The protein can be used in a method of treating a patient in need
 CC of inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis, comprises supplying a fragment,
 CC variant, fusion or derivative of a SNARE or an inhibitory SNARE to the
 CC cell of the patient. The toxin resistant or toxin inhibitory SNARE or a
 CC recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state
 XX Sequence 206 AA;
 SQ
 Query Match 57.0%; Score 49; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 10
 AAE36662
 ID AAE36662 standard; protein; 206 AA.
 XX AAE36662;
 AC AAE36662;
 XX 07-AUG-2003 (first entry)
 DT Human SNAP-25 protein.
 DE Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.

XX Homo sapiens.
OS
XX WO2003020948-A2.
PN
XX
XX
PD 13-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027145.
PF
XX 28-AUG-2001; 2001US-00942024.
PR
XX (ALLR) ALLERGAN INC.
PA
XX Steward LE, Fernandez-Salas E, Aoki KR;
PI
XX WPI; 2003-290198/28.
DR
XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX
PS Claim 6; Page 135-136; 168pp; English.
XX
CC The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysates, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is human
CC SNAP-25 protein used in the invention
XX
SQ Sequence 206 AA;
Query Match 57.0%; Score 49; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
RESULT 11
AAE36667
ID AAE36667 standard; protein; 206 AA.
XX
AC AAE36667;
XX
DT 07-AUG-2003 (first entry)
XX
DE Rat VAMP-2 protein.
XX
XX Rat; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic.
XX
OS Rattus sp.
XX
PN WO2003020948-A2.
XX

PD 13-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027145.
PF
XX 28-AUG-2001; 2001US-00942024.
PR
XX (ALLR) ALLERGAN INC.
PA
XX Steward LE, Fernandez-Salas E, Aoki KR;
PI
XX WPI; 2003-290198/28.
DR
XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX
PS Disclosure; Page 137-138; 168pp; English.
XX
CC The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysates, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is rat VAMP
CC -2 protein used in the invention
XX
SQ Sequence 206 AA;
Query Match 57.0%; Score 49; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
RESULT 12
ADE54280
ID ADE54280 standard; protein; 206 AA.
XX
AC ADE54280;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein BAA20151, SEQ ID NO 83.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR

PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; BAA20151.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially regulated in an animal subjected to pain and a
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 13
 ADE54288
 ID ADE54288 standard; protein; 206 AA.
 XX
 AC ADE54288;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein BAA20152, SEQ ID NO 91.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 FN W02003016475-A2.
 XX
 PD 27-FEB-2003.
 XX

PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; BAA20152.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 14
 ADE54276
 ID ADE54276 standard; protein; 206 AA.
 XX
 AC ADE54276;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein BAA20151, SEQ ID NO 79.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX

DT 29-JAN-2004 (first entry)
 XX Rat Protein BAA20151, SEQ ID NO 85.
 DE
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX WO2003016475-A2.
 PN
 XX 27-FEB-2003.
 PD
 XX 14-AUG-2002; 2002WO-US025765.
 PF
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; BAA20151.
 DR
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 XX Claim 1; Page; 1017pp; English.
 PS
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 17
 ADE54274

ID ADE54274 standard; protein; 206 AA.
 XX
 AC ADE54274;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein BAA20151, SEQ ID NO 77.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX WO2003016475-A2.
 PN
 XX 27-FEB-2003.
 PD
 XX 14-AUG-2002; 2002WO-US025765.
 PF
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; BAA20151.
 DR
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 XX Claim 1; Page; 1017pp; English.
 PS
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
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 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

SQ Sequence 206 AA;

Query Match
Best Local Similarity 57.0%; Score 49; DB 7; Length 206;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 20
ADE54272
ID ADE54272 standard; protein; 206 AA.
XX
AC ADE54272;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein BAA20151, SEQ ID NO 75.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
WPI; 2003-268312/26.
DR GENBANK; BAA20151.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 206 AA;

Query Match
Best Local Similarity 57.0%; Score 49; DB 7; Length 206;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 21
ADE54278
ID ADE54278 standard; protein; 206 AA.
XX
AC ADE54278;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein BAA20151, SEQ ID NO 81.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
WPI; 2003-268312/26.
DR GENBANK; BAA20151.
XX
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PT preparing a medicament for treating pain in an animal.
XX
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CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 86
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 206

RESULT 22
 AAU02640
 ID AAU02640 standard; protein; 206 AA.
 XX
 AC AAU02640;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant L203A.
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 203 /note= "Wild-type Leu substituted by Ala"
 FT
 XX WO200118038-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-GB003196.
 XX
 PR 20-AUG-1999; 99US-0149993P.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX
 DR WPI; 2001-226739/23.
 XX
 PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant L203A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE

CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 206 AA;

Query Match 52.3%; Score 45; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 6.9e-38;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTK 82
 Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTK 202

RESULT 23
 AAU02638
 ID AAU02638 standard; protein; 206 AA.
 XX
 AC AAU02638;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant M202A.
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 202 /note= "Wild-type Met substituted by Ala"
 FT
 XX WO200118038-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-GB003196.
 XX
 PR 20-AUG-1999; 99US-0149993P.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX
 DR WPI; 2001-226739/23.
 XX
 PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant M202A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE

CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
CC a cell of the patient, where the SNARE is resistant to proteolysis by the
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
CC capable of performing SNARE-dependent exocytosis, comprises supplying a
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
CC or a recombinant polynucleotide encoding the SNARE is useful in the
CC manufacture of a medicament for the treatment of a patient suffering from
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
CC botulism or tetanus. The fragment, variant, fusion or derivative of a
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
CC either of these SNARE polypeptides are useful in the manufacture of
CC medicament for the treatment of a patient in need of inhibition of SNARE-
CC dependent exocytosis from a cell capable of performing SNARE-dependent
CC exocytosis. The method of treatment is relatively fast, thus alleviating
CC the symptoms when most severe and taking the patient out of critical
CC state. Note: The present sequence is not shown in the specification but
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
CC AAU00246)
XX
SQ Sequence 206 AA;

Query Match 51.2%; Score 44; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 7.4e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATK 81
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQATK 201

RESULT 24
AAU00255

ID AAU00255 standard; protein; 198 AA.

XX AAU00255;

DT 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.

DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.

XX Mus sp.

OS Synthetic.

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-

CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new
CC method of treating a patient suffering from poisoning or at risk of
CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
CC to a cell of the patient, where the SNARE is resistant to proteolysis by
CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
CC treating a patient in need of inhibition of SNARE-dependent exocytosis
CC from a cell capable of performing SNARE-dependent exocytosis, comprises
CC supplying a fragment, variant, fusion or derivative of a SNARE or an
CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
CC useful in the manufacture of a medicament for the treatment of a patient
CC suffering from poisoning or at risk of poisoning by clostridial toxin,
CC e.g. from botulism or tetanus. The fragment, variant, fusion or
CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
CC polynucleotide encoding either of these SNARE polypeptides are useful in
CC the manufacture of medicament for the treatment of a patient in need of
CC inhibition of SNARE-dependent exocytosis from a cell capable of
CC performing SNARE-dependent exocytosis. The method of treatment is
CC relatively fast, thus alleviating the symptoms when most severe and
CC taking the patient out of critical state. Note: The present sequence is
CC not shown in the specification but is derived from the mouse SNAP-25
CC sequence given in figure 8 (see AAU00246)
XX
SQ Sequence 198 AA;

Query Match 47.7%; Score 41; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 8.5e-34;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 78

Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 198

RESULT 25

AAO15166

ID AAO15166 standard; peptide; 116 AA.

XX AAO15166;

XX 02-SEP-2002 (first entry)

DT Clostridial neurotoxin protease substrate peptide 5.

DE Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
KW fluorescence resonant energy transfer assay; quenched-signal;
KW clostridial neurotoxin detection; food.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "S-fluoresceiny1-cysteine"

FT Cleavage-site 89..90

FT /note= "The peptide is cleaved between these two residues
FT by type E Clostridium botulinum neurotoxin"

XX WO200225284-A2.

XX 28-MAR-2002.

XX 25-SEP-2001; 2001WO-US030188.

XX 25-SEP-2000; 2000US-0235050P.

XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX Schmidt JJ, Stafford RG;

XX WPI; 2002-499829/53.

PT Substrate useful in e.g. an assay for the protease activity of
 XX clostridial neurotoxin, comprises modified peptide or protein.
 PS Claim 28; Page 17; 48pp; English.
 XX
 CC The invention comprises clostridial neurotoxin substrate peptides which
 CC can serve as fluorescence resonant energy transfer assay (FRET) or
 CC quenched-signal substrates in assays for the proteolytic activities of
 CC clostridial neurotoxins. The invention further comprises Clostridium
 CC botulinum neurotoxin substrate peptides that can serve as immobilised
 CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
 CC activities of clostridial neurotoxins. The clostridial (including the
 CC Clostridium botulinum) neurotoxin substrate peptides are useful for
 CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
 CC or an environmental sample). The present amino acid sequence represents a
 CC clostridial neurotoxin substrate peptide of the invention
 XX
 SQ Sequence 116 AA;

Query Match 46.5%; Score 40; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 5.6e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHRMMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 Db 67 GNLHRMMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 106

RESULT 26
 AAU00263
 ID AAU00263 standard; protein; 199 AA.
 XX
 AC AAU00263;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-199(R198T).
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 FT
 XX WO200118038-A2.
 PN
 XX 15-MAR-2001.
 PD
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI
 XX WPI; 2001-226739/23.
 DR
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-199(R198T), used in a new method of

CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

SQ Sequence 199 AA;

Query Match 46.5%; Score 40; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 9e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHRMMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 Db 158 GNLHRMMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 27
 AAU00264
 ID AAU00264 standard; protein; 200 AA.
 XX
 AC AAU00264;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-200(R198T).
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 FT
 XX WO200118038-A2.
 PN
 XX 15-MAR-2001.
 PD
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI
 XX WPI; 2001-226739/23.
 DR
 XX Treating a patient suffering from poisoning or at risk of poisoning by a

PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-200(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX Sequence 200 AA;

Query Match 46.5%; Score 40; DB 4; Length 200;
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 DB 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 28

AAU02637
 ID AAU02637 standard; protein; 201 AA.

AC AAU02637;

DT 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).

KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

OS Mus sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

DR WPI; 2001-226739/23.

XX
 CC Treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, e.g. botulism, comprises administering a toxin-
 CC resistant or toxin-inhibitory SNARE.

PS Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX Sequence 201 AA;

Query Match 46.5%; Score 40; DB 4; Length 201;
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 DB 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 29

AAU00265

ID AAU00265 standard; protein; 202 AA.

AC AAU00265;

DT 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant 1-202(R198T).

KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

OS Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX PD 15-MAR-2001.
 XX XX
 PF 18-AUG-2000; 2000WO-GB003196.
 XX XX
 PR 20-AUG-1999; 99US-0149993P.
 XX XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX XX
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX XX
 DR WPI; 2001-226739/23.
 XX XX
 PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX XX
 PS Example 1; Page; 131pp; English.
 XX XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-202(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX XX
 SQ Sequence 202 AA;
 Query Match 46.5%; Score 40; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 DB 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197
 RESULT 30
 AAU02636
 ID AAU02636 standard; protein; 203 AA.
 XX
 AC AAU02636;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-203 (R198T).
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 XX
 PN WO200118038-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-GB003196.
 XX
 PR 20-AUG-1999; 99US-0149993P.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX
 DR WPI; 2001-226739/23.
 XX
 PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 203 AA;
 Query Match 46.5%; Score 40; DB 4; Length 203;
 Best Local Similarity 100.0%; Pred. No. 9.2e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 DB 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197
 RESULT 31
 AAU00261
 ID AAU00261 standard; protein; 206 AA.
 XX
 AC AAU00261;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant R198A.
 XX

KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX
OS Mus sp.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 198 /note= "Wild-type Arg substituted by Ala"
XX
XX WO200118038-A2.
XX
XX 15-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-GB003196.
XX
XX 20-AUG-1999; 99US-0149993P.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
XX
XX WPI; 2001-226739/23.
XX
XX Treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, e.g. botulism, comprises administering a toxin-
XX resistant or toxin-inhibitory SNARE.
XX
XX Example 1; Page; 131pp; English.
XX
XX The sequence represents the amino acid sequence of synaptosomal-
XX associated protein, SNAP25, mutant R198A used in a new method of treating
XX a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, comprising supplying a SNARE (soluble (N-
XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
XX a cell of the patient, where the SNARE is resistant to proteolysis by the
XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
XX capable of performing SNARE-dependent exocytosis, comprises supplying a
XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
XX or a recombinant polynucleotide encoding the SNARE is useful in the
XX manufacture of a medicament for the treatment of a patient suffering from
XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
XX botulism or tetanus. The fragment, variant, fusion or derivative of a
XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
XX either of these SNARE polypeptides are useful in the manufacture of
XX medicament for the treatment of a patient in need of inhibition of SNARE-
XX dependent exocytosis from a cell capable of performing SNARE-dependent
XX exocytosis. The method of treatment is relatively fast, thus alleviating
XX the symptoms when most severe and taking the patient out of critical
XX state. Note: The present sequence is not shown in the specification but
XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
XX AAU00246)
XX
SQ Sequence 206 AA;

Query Match 46.5%; Score 40; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.3e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLWALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
Db 158 GNLRLWALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 32
AAU02171
ID AAU02171 standard; protein; 206 AA.

XX
AC AAU02171;
XX
XX 12-SEP-2001 (first entry)
XX
XX Synaptosomal-associated protein, SNAP25, mutant R198T/L203A.
XX
XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX
XX Mus sp.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
XX Misc-difference 203 /note= "Wild-type Leu substituted by Ala"
XX
XX WO200118038-A2.
XX
XX 15-MAR-2001.
XX
XX 18-AUG-2000; 2000WO-GB003196.
XX
XX 20-AUG-1999; 99US-0149993P.
XX
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
XX
XX WPI; 2001-226739/23.
XX
XX Treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, e.g. botulism, comprises administering a toxin-
XX resistant or toxin-inhibitory SNARE.
XX
XX Example 1; Page; 131pp; English.
XX
XX The sequence represents the amino acid sequence of synaptosomal-
XX associated protein, SNAP25, mutant R198T/L203A, used in a new method of
XX treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, comprising supplying a SNARE (soluble (N-
XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
XX a cell of the patient, where the SNARE is resistant to proteolysis by the
XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
XX capable of performing SNARE-dependent exocytosis, comprises supplying a
XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
XX or a recombinant polynucleotide encoding the SNARE is useful in the
XX manufacture of a medicament for the treatment of a patient suffering from
XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
XX botulism or tetanus. The fragment, variant, fusion or derivative of a
XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
XX either of these SNARE polypeptides are useful in the manufacture of
XX medicament for the treatment of a patient in need of inhibition of SNARE-
XX dependent exocytosis from a cell capable of performing SNARE-dependent
XX exocytosis. The method of treatment is relatively fast, thus alleviating
XX the symptoms when most severe and taking the patient out of critical
XX state. Note: The present sequence is not shown in the specification but
XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
XX AAU00246)
XX
SQ Sequence 206 AA;

Query Match 46.5%; Score 40; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.3e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 DB 158 GNLRLMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 33

AAU00259
 ID AAU00259 standard; protein; 206 AA.

AC AAU00259;

XX 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant R198T.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

OS Mus sp.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX 15-MAR-2001.

PF 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

PS Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant R198T used in a new method of treating
 CC a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see

CC AAU00246)

XX Sequence 206 AA;

Query Match 46.5%; Score 40; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.3e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77

DB 158 GNLRLMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 34

AAU02639

ID AAU02639 standard; protein; 206 AA.

XX AAU02639;

DT 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant R198T/M202A.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

OS Mus sp.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Thr"

FT Misc-difference 202

FT /note= "Wild-type Met substituted by Ala"

XX WO200118038-A2.

XX 15-MAR-2001.

PF 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

PS Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant R198T/M202A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from

CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX Sequence 206 AA;

SQ Query Match 46.5%; Score 40; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.3e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 Db 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 35
 AAU00256
 ID AAU00256 standard; protein; 206 AA.

XX AC AAU00256;
 XX DT 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, mutant Q197A/R198A.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Ala"
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Ala"

XX WO200118038-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX DR WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant Q197A/R198A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the

CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX Sequence 206 AA;

SQ Query Match 45.3%; Score 39; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.9e-32;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
 Db 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 36
 AAU00266
 ID AAU00266 standard; protein; 206 AA.

XX AC AAU00266;
 XX DT 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, mutant Q197K/R198H.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Lys"
 FT Misc-difference 198 /note= "Wild-type Arg substituted by His"

XX WO200118038-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

XX PS Example 1; Page; 131pp; English.

XX CC The sequence represents the amino acid sequence of synaptosomal-

CC associated protein, SNAP25, mutant Q197K/R198H, used in a new method of

CC treating a patient suffering from poisoning or at risk of poisoning by a

CC clostridial toxin, comprising supplying a SNARE (soluble (N-

CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to

CC a cell of the patient, where the SNARE is resistant to proteolysis by the

CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin

CC (toxin-inhibitory SNARE). The protein can be used in a method of treating

CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell

CC capable of performing SNARE-dependent exocytosis, comprises supplying a

CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE

CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE

CC or a recombinant polynucleotide encoding the SNARE is useful in the

CC manufacture of a medicament for the treatment of a patient suffering from

CC poisoning or at risk of poisoning by clostridial toxin, e.g. from

CC botulism or tetanus. The fragment, variant, fusion or derivative of a

CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding

CC either of these SNARE polypeptides are useful in the manufacture of

CC medicament for the treatment of a patient in need of inhibition of SNARE-

CC dependent exocytosis from a cell capable of performing SNARE-dependent

CC exocytosis. The method of treatment is relatively fast, thus alleviating

CC the symptoms when most severe and taking the patient out of critical

CC state. Note: The present sequence is not shown in the specification but

CC is derived from the mouse SNAP-25 sequence given in figure 8 (see

CC AAU00246)

XX SQ Sequence 206 AA;

Query Match 45.3%; Score 39; DB 4; Length 206;

Best Local Similarity 100.0%; Pred. No. 9.9e-32;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76

Db 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 37

AAU00258

ID AAU00258 standard; protein; 206 AA.

XX AC AAU00258;

DT 12-SEP-2001 (first entry)

XX DE Synaptosomal-associated protein, SNAP25, mutant Q197W/R198W.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;

KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;

KW synaptosomal-associated protein; mouse; mutant; mutein;

KW N-ethylmaleimide-sensitive fusion protein;

KW soluble NSF-attachment protein receptor.

XX OS Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 197 /note= "Wild-type Gln substituted by Trp"

FT Misc-difference 198 /note= "Wild-type Arg substituted by Trp"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;

PI WPI; 2001-226739/23.

DR

XX Treating a patient suffering from poisoning or at risk of poisoning by a

PT clostridial toxin, e.g. botulism, comprises administering a toxin-

PT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-

CC associated protein, SNAP25, mutant Q197W/R198W, used in a new method of

CC treating a patient suffering from poisoning or at risk of poisoning by a

CC clostridial toxin, comprising supplying a SNARE (soluble (N-

CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to

CC a cell of the patient, where the SNARE is resistant to proteolysis by the

CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin

CC (toxin-inhibitory SNARE). The protein can be used in a method of treating

CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell

CC capable of performing SNARE-dependent exocytosis, comprises supplying a

CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE

CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE

CC or a recombinant polynucleotide encoding the SNARE is useful in the

CC manufacture of a medicament for the treatment of a patient suffering from

CC poisoning or at risk of poisoning by clostridial toxin, e.g. from

CC botulism or tetanus. The fragment, variant, fusion or derivative of a

CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding

CC either of these SNARE polypeptides are useful in the manufacture of

CC medicament for the treatment of a patient in need of inhibition of SNARE-

CC dependent exocytosis from a cell capable of performing SNARE-dependent

CC exocytosis. The method of treatment is relatively fast, thus alleviating

CC the symptoms when most severe and taking the patient out of critical

CC state. Note: The present sequence is not shown in the specification but

CC is derived from the mouse SNAP-25 sequence given in figure 8 (see

CC AAU00246)

XX SQ Sequence 206 AA;

Query Match 45.3%; Score 39; DB 4; Length 206;

Best Local Similarity 100.0%; Pred. No. 9.9e-32;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76

Db 158 GNLRLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 38

AAU00262

ID AAU00262 standard; protein; 206 AA.

XX AC AAU00262;

DT 12-SEP-2001 (first entry)

XX DE Synaptosomal-associated protein, SNAP25, mutant Q197K/R198K.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;

KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;

KW synaptosomal-associated protein; mouse; mutant; mutein;

KW N-ethylmaleimide-sensitive fusion protein;

KW soluble NSF-attachment protein receptor.

XX OS Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 197 /note= "Wild-type Gln substituted by Lys"

FT Misc-difference 198 /note= "Wild-type Arg substituted by Lys"

XX WO200118038-A2.
XX 15-MAR-2001.
XX 18-AUG-2000; 2000WO-GB003196.
XX 20-AUG-1999; 99US-0149993P.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
XX WPI; 2001-226739/23.
XX Treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, e.g. botulism, comprises administering a toxin-
XX resistant or toxin-inhibitory SNARE.
XX Example 1; Page; 131pp; English.
XX The sequence represents the amino acid sequence of synaptosomal-
XX associated protein, SNAP25, mutant Q197K/R198K, used in a new method of
XX treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, comprising supplying a SNARE (soluble (N-
XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
XX a cell of the patient, where the SNARE is resistant to proteolysis by the
XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
XX capable of performing SNARE-dependent exocytosis, comprises supplying a
XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
XX or a recombinant polynucleotide encoding the SNARE is useful in the
XX manufacture of a medicament for the treatment of a patient suffering from
XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
XX botulism or tetanus. The fragment, variant, fusion or derivative of a
XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
XX medicament for the treatment of a patient in need of inhibition of SNARE-
XX dependent exocytosis from a cell capable of performing SNARE-dependent
XX exocytosis. The method of treatment is relatively fast, thus alleviating
XX the symptoms when most severe and taking the patient out of critical
XX state. Note: The present sequence is not shown in the specification but
XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
XX AAU00246)
XX Sequence 206 AA;
XX Query Match 45.3%; Score 39; DB 4; Length 206;
XX Best Local Similarity 100.0%; Pred. No. 9.9e-32;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
RESULT 39
AAU00260
ID AAU00260 standard; protein; 206 AA.
AC AAU00260;
XX 12-SEP-2001 (first entry)
XX Synaptosomal-associated protein, SNAP25, mutant Q197A.
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.

XX Mus sp.
OS Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 197 /note= "Wild-type Gln substituted by Ala"
XX WO200118038-A2.
XX 15-MAR-2001.
XX 18-AUG-2000; 2000WO-GB003196.
XX 20-AUG-1999; 99US-0149993P.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
XX WPI; 2001-226739/23.
XX Treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, e.g. botulism, comprises administering a toxin-
XX resistant or toxin-inhibitory SNARE.
XX Example 1; Page; 131pp; English.
XX The sequence represents the amino acid sequence of synaptosomal-
XX associated protein, SNAP25, mutant Q197A, used in a new method of
XX treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, comprising supplying a SNARE (soluble (N-
XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
XX a cell of the patient, where the SNARE is resistant to proteolysis by the
XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
XX capable of performing SNARE-dependent exocytosis, comprises supplying a
XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
XX or a recombinant polynucleotide encoding the SNARE is useful in the
XX manufacture of a medicament for the treatment of a patient suffering from
XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
XX botulism or tetanus. The fragment, variant, fusion or derivative of a
XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
XX either of these SNARE polypeptides are useful in the manufacture of
XX medicament for the treatment of a patient in need of inhibition of SNARE-
XX dependent exocytosis from a cell capable of performing SNARE-dependent
XX exocytosis. The method of treatment is relatively fast, thus alleviating
XX the symptoms when most severe and taking the patient out of critical
XX state. Note: The present sequence is not shown in the specification but
XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
XX AAU00246)
XX Sequence 206 AA;
XX Query Match 45.3%; Score 39; DB 4; Length 206;
XX Best Local Similarity 100.0%; Pred. No. 9.9e-32;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
RESULT 40
AAU00257
ID AAU00257 standard; protein; 206 AA.
XX AAU00257;
AC AAU00257;
XX 12-SEP-2001 (first entry)
XX

DE XX Synaptosomal-associated protein, SNAP25, mutant Q197A/R198K.
XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX Mus sp.
OS Synthetic.
OS Key Location/Qualifiers
XX Misc-difference 197 /note= "Wild-type Gln substituted by Ala"
FT Misc-difference 198 /note= "Wild-type Arg substituted by Lys"
FT
XX WO200118038-A2.
PN 15-MAR-2001.
XX 18-AUG-2000; 2000WO-GB003196.
PF 20-AUG-1999; 99US-0149993P.
PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
PI WPI; 2001-226739/23.
DR
XX Treating a patient suffering from poisoning or at risk of poisoning by a
PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.
XX Example 1; Page; 131pp; English.
XX The sequence represents the amino acid sequence of synaptosomal-
CC associated protein, SNAP25, mutant Q197A/R198K, used in a new method of
CC treating a patient suffering from poisoning or at risk of poisoning by a
CC clostridial toxin, comprising supplying a SNARE (soluble (N-
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
CC a cell of the patient, where the SNARE is resistant to proteolysis by the
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
CC capable of performing SNARE-dependent exocytosis, comprises supplying a
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
CC or a recombinant polynucleotide encoding the SNARE is useful in the
CC manufacture of a medicament for the treatment of a patient suffering from
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
CC botulism or tetanus. The fragment, variant, fusion or derivative of a
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
CC either of these SNARE polypeptides are useful in the manufacture of
CC medicament for the treatment of a patient in need of inhibition of SNARE-
CC dependent exocytosis from a cell capable of performing SNARE-dependent
CC exocytosis. The method of treatment is relatively fast, thus alleviating
CC the symptoms when most severe and taking the patient out of critical
CC state. Note: The present sequence is not shown in the specification but
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
CC AAU00246)
XX SQ Sequence 206 AA;
Query Match 45.3%; Score 39; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.9e-32;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
Db 158 GNLRHMLDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 41
AAW30097
ID AAW30097 standard; peptide; 37 AA.
XX
AC AAW30097;
XX 06-APR-1998 (first entry)
DT
XX Neurotransmitter secretion inhibitor #1.
DE
XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
KW excitation-secretory uncoupling peptide; catecholamine secretion;
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
KW synaptosomal associated protein; SNAP-25.
XX
OS Homo sapiens.
XX WO9734620-A1.
PN 25-SEP-1997.
PD
XX 18-MAR-1997; 97WO-US004393.
PF 18-MAR-1996; 96US-0013599P.
PR (REGC) UNIV CALIFORNIA.
XX Montal M;
PI WPI; 1997-479986/44.
DR
XX Excitation-secretory uncoupling peptide(s) for inhibiting
PT neuro-transmitter release - used particularly for treating muscle
PT spasticity, and for delivering drugs specifically to neural cells.
XX
PS Claim 1; Page 30; 61pp; English.
XX This sequence corresponds to residues 170-206 of the human 25 kD
CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of
CC the invention. The agents of the invention inhibit secretion of
CC neurotransmitter from neuronal cells and is an excitation-secretory
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
CC correspond substantially to any one of AAW30097-W30102, or more generally
CC any (I) that inhibits 50% of catecholamine secretion from bovine
CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,
CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
CC release of neurotransmitters from synaptic vesicles, specifically for
CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
CC imaging of intracellular distribution of (I). Compounds for delivering
CC the drug to neural cells provide targeted drug delivery, e.g. of
CC substance P to brain tumours for induction of apoptosis. Unlike the
CC neurotoxins, (I) are not toxic or immunogenic and are more readily
CC available. Their therapeutic effect lasts for several days or weeks, so
CC lower doses or less frequent treatments are required
XX SQ Sequence 37 AA;
Query Match 43.0%; Score 37; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.4e-30;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 EIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 86
Db 1 EIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 37
RESULT 42
AAE36683
ID AAE36683 standard; peptide; 33 AA.
XX
AC AAE36683;
XX

DT 07-AUG-2003 (first entry)
XX Goldfish SNAP-25B peptide.
DE Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT; BoNT;
XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW TeNT; cosmetic.
KW Carassius auratus.
XX Key Location/Qualifiers
OS Cleavage-site 7. .8 /note= "BoNT/E sensitive cleavage site"
FT Cleavage-site 24. .25 /note= "BoNT/A sensitive cleavage site"
FT Cleavage-site 25. .26 /note= "BoNT/C sensitive cleavage site"
FT WO2003020948-A2.
XX 13-MAR-2003.
XX 22-AUG-2002; 2002WO-US027145.
XX 28-AUG-2001; 2001US-00942024.
XX (ALLR) ALLERGAN INC.
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-290198/28.
XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX Disclosure; Page 42; 168pp; English.
XX The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is goldfish
CC SNAP-25B peptide used in the invention
XX Sequence 33 AA;
SQ
Query Match 38.4%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.7e-26;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 1 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33
RESULT 43
AAE36678
ID AAE36678 standard; peptide; 33 AA.

XX AAE36678;
AC 07-AUG-2003 (first entry)
DT SNAP-25 peptide.
XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
KW cosmetic; mouse; rat.
XX Homo sapiens.
OS Mus musculus.
OS Rattus sp.
FH Key Location/Qualifiers
FT Cleavage-site 7. .8 /note= "BoNT/E sensitive cleavage site"
FT Cleavage-site 24. .25 /note= "BoNT/A sensitive cleavage site"
FT Cleavage-site 25. .26 /note= "BoNT/C sensitive cleavage site"
FT WO2003020948-A2.
XX 13-MAR-2003.
XX 22-AUG-2002; 2002WO-US027145.
XX 28-AUG-2001; 2001US-00942024.
XX (ALLR) ALLERGAN INC.
XX Steward LE, Fernandez-Salas E, Aoki KR;
XX WPI; 2003-290198/28.
XX Botulinum serotype A/E substrate useful for assaying protease activity of
PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
PT toxin recognition sequence that includes a cleavage site.
XX Disclosure; Page 42; 168pp; English.
XX The present invention relates to novel clostridium toxin substrates. The
CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
CC which comprise a donor fluorophore, an acceptor having an absorbance
CC spectrum overlapping the emission spectrum of the donor fluorophore and a
CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
CC the cleavage site intervenes between the donor fluorophore and acceptor
CC and under the appropriate conditions, the resonance energy transfer is
CC exhibited between the donor and acceptor. Natural targets of clostridium
CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
CC of the invention are useful in assaying for the protease activity of any
CC clostridial toxin including botulinum toxins of all serotypes and tetanus
CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
CC samples, water samples, cosmetics, tissue samples and beverage or food
CC samples. They are useful to assay a sample from a human or animal, for
CC e.g., exposed to clostridial toxin or having one or more symptoms of a
CC clostridial toxin, to follow activity during production and purification
CC of clostridial toxin and to assay formulated clostridial toxin products
CC including pharmaceuticals and cosmetics. The present sequence is SNAP-25
CC peptide used in the invention
XX Sequence 33 AA;
SQ
Query Match 38.4%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.7e-26;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 1 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33

us-10-030-485a-4.rag

Fri Mar 5 07:11:12 2004

bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.

kw bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synaptosomal associated protein; SNAP-25.
xx Homo sapiens.
xx WO9734620-A1.
xx 25-SEP-1997.
xx 18-MAR-1997; 97WO-US004393.
xx 18-MAR-1996; 96US-0013599P.
xx (REGC) UNIV CALIFORNIA.
xx Montal M;
xx WPI; 1997-479986/44.
xx Excitation-secretory uncoupling peptide(s) for inhibiting neuro:transmitter release - used particularly for treating muscle spasticity, and for delivering drugs specifically to neural cells.
xx Claim 13; Page 31; 61pp; English.
xx This sequence corresponds to residues 181-206 of the human 25 kD synaptosomal associated protein (SNAP-25), and is an inhibitory agent of the invention. The agents of the invention inhibit secretion of neurotransmitter from neuronal cells and is an excitation-secretory uncoupling peptide (I) of at least 20 amino acids (aa) all of which correspond substantially to any one of AAW30097-W30102, or more generally any (I) that inhibits 50% of catecholamine secretion from bovine chromaffin cells at a concentration of 10 microm, especially 0.25 microm, or less. (I) are used, as a replacement for Clostridium toxin, to inhibit release of neurotransmitters from synaptic vesicles, specifically for reducing muscle spasticity. Also (I) may be labelled to allow in vivo imaging of intracellular distribution of (I). Compounds for delivering the drug to neural cells provide targeted drug delivery, e.g. of substance P to brain tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not toxic or immunogenic and are more readily available. Their therapeutic effect lasts for several days or weeks, so lower doses or less frequent treatments are required

Sequence 26 AA;

Query Match 30.2%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 IMEKADSNKTRIDEANQRATKMLGSG 86
Db 1 IMEKADSNKTRIDEANQRATKMLGSG 26

Search completed: March 4, 2004, 08:32:52
Job time : 55 secs

RESULT 44
AAW57386
ID AAW57386 standard; protein; 49 AA.
xx AAW57386;
xx 05-NOV-2001 (first entry)
xx Human brain expressed single exon probe encoded protein SEQ ID NO: 29491.
xx Human; brain expressed exon; gene expression analysis; probe; microarray;
xx Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
xx Homo sapiens.
xx WO200157275-A2.
xx 09-AUG-2001.
xx 30-JAN-2001; 2001WO-US000667.
xx 04-FEB-2000; 2000US-0180312P.
xx 26-MAY-2000; 2000US-0207456P.
xx 30-JUN-2000; 2000US-00608408.
xx 03-AUG-2000; 2000US-00632366.
xx 21-SEP-2000; 2000US-0234687P.
xx 27-SEP-2000; 2000US-0236359P.
xx 04-OCT-2000; 2000GB-00024263.
xx (MOLE-) MOLECULAR DYNAMICS INC.
xx Penn SG, Hanzel DK, Chen W, Rank DR;
xx WPI; 2001-483446/52.
xx Single exon nucleic acid probes for analyzing gene expression in human brains.

Example 4; SEQ ID NO 29491; 650pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention

Sequence 49 AA;

Query Match 31.4%; Score 27; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.5e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLEHMDMGNEIDTQNRQIDRIMEX 64
Db 22 GNLEHMDMGNEIDTQNRQIDRIMEX 48

RESULT 45
AAW30099
ID AAW30099 standard; peptide; 26 AA.
xx AAW30099;
xx 06-APR-1998 (first entry)
xx Neurotransmitter secretion inhibitor #3.
xx Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
xx excitation-secretory uncoupling peptide; catecholamine secretion;

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 48.5789 Seconds
(without alignments)
84.434 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEMQRADQLA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	206	13	Q8AXM2
2	62	100.0	206	13	Q8AXM1
3	57	91.9	18	6	Q9TRF1
4	45	72.6	794	5	Q7YY86
5	44	71.0	55	13	Q93580
6	44	71.0	203	13	Q93579
7	44	71.0	252	16	Q99YW2
8	44	71.0	252	16	Q8K6S1
9	44	71.0	701	11	Q7TS27
10	42	67.7	1034	10	Q93X69
11	41	66.1	201	16	Q88DN0
12	41	66.1	253	11	Q9WV62
13	41	66.1	315	9	Q9G050
14	41	66.1	480	17	Q9UYW5
15	41	66.1	664	17	Q9HN61
16	41	66.1	698	16	Q8XQ05

17	40	64.5	149	16	Q92B51
18	40	64.5	885	11	Q8BLI3
19	40	64.5	998	11	Q8BLI1
20	40	64.5	1833	11	Q80T68
21	40	64.5	1999	11	Q63731
22	40	64.5	2007	13	Q02015
23	40	64.5	2107	5	Q18736
24	40	64.5	5362	2	Q93I55
25	39	62.9	91	5	Q9XYH9
26	39	62.9	119	16	Q8CYA6
27	39	62.9	156	4	Q8TER8
28	39	62.9	190	16	Q9PGZ4
29	39	62.9	248	16	Q886J4
30	39	62.9	265	16	Q89HF5
31	39	62.9	437	4	Q8N8Y0
32	39	62.9	442	4	Q9BZD5
33	39	62.9	442	4	Q9BX97
34	39	62.9	455	4	Q86VP0
35	39	62.9	456	4	Q8ND68
36	39	62.9	476	6	Q9GMV3
37	39	62.9	532	5	Q61745
38	39	62.9	565	5	Q95TY5
39	39	62.9	630	5	Q9VF74
40	39	62.9	652	11	Q8BREF
41	39	62.9	658	5	Q86NV7
42	39	62.9	675	12	Q8JS27
43	39	62.9	740	16	Q9RKJ0
44	39	62.9	1166	4	Q86YT3
45	39	62.9	1209	6	Q8MI28

ALIGNMENTS

RESULT 1

Q8AXM2 ID Q8AXM2 PRELIMINARY; PRT; 206 AA.
AC Q8AXM2;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE SNAP25a.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335586; AAO13788.1; -
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; T-SNARE; 2.
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match 100.0%; Score 62; DB 13; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELEMQRADQLA 13
Db 10 ELEMQRADQLA 22

RESULT 2

Q8AXM1 ID Q8AXM1 PRELIMINARY; PRT; 206 AA.
AC Q8AXM1;

DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE SNAP25b (Hypothetical protein).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF335587; AA03789.1; -;
 DR EMBL; BC055981; AAH55981.1; -;
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS50192; T_SNARE; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;

Query Match 100.0%; Score 62; DB 13; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
 |||||
 Db 10 ELEMQRADQLA 22

RESULT 3
 Q9TRF1

ID Q9TRF1 PRELIMINARY; PRT; 18 AA.
 AC Q9TRF1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE Soluble N-ethylmaleimide-sensitive attachment protein SNAP-25
 DE (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93374072; PubMed=8365494;
 RA Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tsugita A., Odani S.,
 RA Abe T.;
 RL FEBS Lett. 330:236-240(1993).
 SQ SEQUENCE 18 AA; 2120 MW; 371FC93766C4A7BB CRC64;

Query Match 91.9%; Score 57; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEEMQRADQLA 13
 |||||
 Db 1 LEEMQRADQLA 12

RESULT 4

QY Y86 PRELIMINARY; PRT; 794 AA.
 AC QY Y86;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Asparagine-rich protein, possible.
 GN 1MB.390.
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 OX NCBI_TaxID=5807;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Iowa;
 RA Bankier A.T., Spriggs H.F., Partmann B., Konfortov B.A., Madera M.,
 RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
 RT "Integrated mapping, chromosomal sequencing and sequence analysis of
 RT Cryptosporidium parvum.";
 RL Genome Res. 0:0-0(2003).
 DR EMBL; BX58351; CAD98599.1; -;
 SQ SEQUENCE 794 AA; 92848 MW; 37E6DF58F62A5358 CRC64;

Query Match 72.6%; Score 45; DB 5; Length 794;
 Best Local Similarity 61.5%; Pred. No. 71;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
 |||||
 Db 777 EIEELQREDELA 789

RESULT 5

O93580 PRELIMINARY; PRT; 55 AA.
 AC O93580;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Synaptosome-associated protein 25.2 (Fragment).
 GN SNAP25B OR SNAP.

OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99057281; PubMed=9843147;
 RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Larhammar D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage."
 RL J. Neurosci. Res. 54:563-573 (1998).
 DR EMBL; AF091595; AAC64291.1; -
 DR ZFIN; ZDB-GENE-980526-392; snap25b.
 FT NON TER 55
 SQ SEQUENCE 55 AA; 6200 MW; 7ABE9C2D3590AB9 CRC64;
 Query Match 71.0%; Score 44; DB 13; Length 55;
 Best Local Similarity 75.0%; Pred. No. 8.4;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ELEMQRADQL 12
 Db 10 ELNDMQARADQL 21
 RESULT 6
 O93579
 ID O93579 PRELIMINARY; PRT; 203 AA.
 AC O93579;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein
 DE 25.2).
 GN SNAP25B OR SNAP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Larhammar D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage."
 RL J. Neurosci. Res. 0:0-0 (1998).
 DR EMBL; AF091594; AAC64290.1; -
 DR EMBL; AF091596; AAC73007.1; -
 DR ZFIN; ZDB-GENE-980526-392; snap25b.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T-SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS0192; T-SNARE; 2.
 SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
 Query Match 71.0%; Score 44; DB 13; Length 203;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ELEMQRADQL 12
 Db 10 ELNDMQARADQL 21
 RESULT 7
 Q99YW2
 ID Q99YW2 PRELIMINARY; PRT; 252 AA.
 AC Q99YW2;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cell-division initiation protein (Septum placement).
 GN DIVIVAS OR SPY1514 OR SPYM18_1532.
 OS Streptococcus pyogenes, and
 OS Streptococcus pyogenes (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314, 186103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108;
 RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
 DR EMBL; AE006585; AAK34310.1; -
 DR EMBL; AE010068; AAL98100.1; -
 DR InterPro; IPR007793; DivIVA.
 DR Pfam; PF05103; DivIVA; 1.
 KW Complete proteome.
 SQ SEQUENCE 252 AA; 28934 MW; EB8BC08994AB2CDC CRC64;
 Query Match 71.0%; Score 44; DB 16; Length 252;
 Best Local Similarity 72.7%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ELEMQRADQL 11
 Db 208 ELEELQRRVDE 218
 RESULT 8
 O8K6S1
 ID O8K6S1 PRELIMINARY; PRT; 252 AA.
 AC O8K6S1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative cell-division initiation protein (Septum placement).
 GN DIVIVA OR SPYM3_1167 OR SPS0695.
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=198466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206;
 RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).


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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Taniyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014159; AAM79774.1; -.
DR EMBL; AP005143; BAC63790.1; -.
DR InterPro; IPR007793; DivIVA.
DR Pfam; PF05103; DivIVA; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 252 AA; 28938 MW; EB8C08994AB29C8 CRC64;

Query Match 71.0%; Score 44; DB 16; Length 252;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQ 11
Db 208 ELEELQRRVDE 218

RESULT 9
Q7TSZ7
ID Q7TSZ7 PRELIMINARY; PRT; 701 AA.
AC Q7TSZ7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kif3a protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettnerman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052707; AAH52707.1; -.
SQ SEQUENCE 701 AA; 80169 MW; 15EB43A6F6CC08A3 CRC64;

Query Match 71.0%; Score 44; DB 11; Length 701;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Taniyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014159; AAM79774.1; -.
DR EMBL; AP005143; BAC63790.1; -.
DR InterPro; IPR007793; DivIVA.
DR Pfam; PF05103; DivIVA; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 252 AA; 28938 MW; EB8C08994AB29C8 CRC64;

Query Match 71.0%; Score 44; DB 16; Length 252;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQ 12
Db 505 ELEERRRAEQL 516

RESULT 10
Q93X69 PRELIMINARY; PRT; 1034 AA.
AC Q93X69;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NBS-LRR-like protein.
GN YR9.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Yuxi 2; TISSUE=Leaf;
RA Yang Q.Z., Yang P.W., Wang Q., Liu J.M., Cheng Z.Q., Yan B., Li J.R.,
RA Huang X.Q.;
RT "Molecular cloning of a novel cDNA encoding a nucleotide-binding site
RT and leucine-rich repeats from rice seedling leaf."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY043283; AAK93796.1; -.
DR Gramene; Q93X69; -.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0003793; F-defense/immunity protein activity; IEA.
DR GO; GO:0006915; P-apoptosis; IEA.
DR GO; GO:0006952; P-defense response; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR; 2.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERSIST.
SQ SEQUENCE 1034 AA; 116268 MW; 0985AEB991E9A0B6 CRC64;

Query Match 67.7%; Score 42; DB 10; Length 1034;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRAD 10
Db 33 ELEELQRRTD 42

RESULT 11
Q88DN0 PRELIMINARY; PRT; 201 AA.
AC Q88DN0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Lipoprotein, putative.
GN PP4795.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

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RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;

RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile *Pseudomonas putida* KT2440.";

RL Environ. Microbiol. 4:799-808(2002).

DR EMBL; AE016792; AAN70364.1; -.

DR TIGR; PP4795; -.

DR InterPro; IPR000437; Prok_lipoprot_S.

DR InterPro; IPR007485; RplB.

DR Pfam; PF04390; RplB; 1.

DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

KW Complete proteome.

SQ SEQUENCE 201 AA; 22414 MW; BEE46C36E59A65BE CRC64;

Query Match 66.1%; Score 41; DB 16; Length 201;

Best Local Similarity 53.8%; Pred. No. 84;

Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13

:|:|:|:|:|

Db 161 QLDELQKADERA 173

RESULT 12

Q9WV62

ID Q9WV62 PRELIMINARY; PRT; 253 AA.

AC Q9WV62;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Kinesin-like protein KIF3A (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Gould R.M., Freund C.M., Hawkins G.A.;

RT "Rat kinesin probes to use for Northern blot analysis.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF155825; AAD39242.1; -.

FT NON_TER 1

FT NON_TER 253

SQ SEQUENCE 253 AA; 30104 MW; 5A61CE5F5B94B44 CRC64;

Query Match

Best Local Similarity 66.1%; Score 41; DB 11; Length 253;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12

||||:|:|:|

Db 113 ELEERRKRAEQL 124

RESULT 13

Q9G050

ID Q9G050 PRELIMINARY; PRT; 315 AA.

AC Q9G050;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE Vp4.

OS Phage phiMH2K.

OC Viruses; ssDNA viruses; Microviridae; Microvirus.

OC NCBI_TaxID=145579;

RN [1]

RP SEQUENCE FROM N.A.

RA Fane B.A., Hafenstein S.L., Brentlinger K.L., Burch A.D., Novak C.R.;

RT "The complete genome sequence of the a Microviridae virus, phiMH2K,

RT isolated from Bdellovirio Bacteriovorus.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF306496; AAG45349.1; -.

SQ SEQUENCE 315 AA; 37231 MW; EB0BC61D3CF67BFB CRC64;

Query Match 66.1%; Score 41; DB 9; Length 315;

Best Local Similarity 75.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12

||||:|:|:|

Db 264 ELAEMQSRKQDL 275

RESULT 14

Q9UYW5

ID Q9UYW5 PRELIMINARY; PRT; 480 AA.

AC Q9UYW5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein PYRAB13920.

GN PYRAB13920 OR PAB1455.

OS Pyrococcus abyssi.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

OC Pyrococcus.

OC NCBI_TaxID=29292;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GES / Orsay;

RA Heilig R.;

RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome

RT structure and evolution.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ248287; CAB50297.1; -.

DR PIR; D75050; D75050.

DR InterPro; IPR007509; DUF515.

DR Pfam; PF04415; DUF515; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 480 AA; 53536 MW; F10B305BC854B981 CRC64;

Query Match

Best Local Similarity 66.1%; Score 41; DB 17; Length 480;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12

||||:|:|:|

Db 150 ELEAKRRABEL 161

RESULT 15

Q9HN61

ID Q9HN61 PRELIMINARY; PRT; 664 AA.

AC Q9HN61;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Vng2238c.

GN VNG2238c.

OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).

OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;

OC Halobacteriaceae; Halobacterium.

OC NCBI_TaxID=64091;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20504483; PubMed=11016950;

RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Sbrogna J.,

RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;

RT "Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

RL

DR EMEL; AE005109; AAG20360.1; -.
 DR PIR; D84374; D84374.
 DR InterPro; IPR001395; Aldo/ket_red.
 DR InterPro; IPR007408; DUF460.
 DR Pfam; PF04312; DUF460; 1.
 DR PROSITE; PS00063; ALDO-KETO-REDUCTASE_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 664 AA; 73964 MW; 708B778DB502269B CRC64;

Query Match 66.1%; Score 41; DB 17; Length 664;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEEMQRRADQL 12
 ||||:||||
 Db 494 ELEEQRRADEL 505

Search completed: March 4, 2004, 08:29:16
 Job time : 50.5789 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 14.3684 Seconds
(without alignments)
47.111 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEMQRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	206	1 SN25 HUMAN	P13795 homo sapien
2	50	80.6	204	1 SN2A_CARAU	P36977 carassius a
3	44	71.0	701	1 KF3A_MOUSE	P28741 mus musculu
4	43	69.4	203	1 SN2B_CARAU	P36978 carassius a
5	42	67.7	210	1 SN25 TORMA	P36976 torpedo mar
6	41	66.1	157	1 PFDA_METKA	Q8tuy7 methanopyru
7	41	66.1	702	1 KF3A_HUMAN	Q9Y496 homo sapien
8	40	64.5	102	1 VAM5_RAT	Q9Z2J5 rattus norv
9	40	64.5	1976	1 MYHA_BOVIN	Q27991 bos taurus
10	40	64.5	1976	1 MYHA_HUMAN	P35580 homo sapien
11	40	64.5	1976	1 MYHA_RAT	Q9Jlt0 rattus norv
12	40	64.5	2107	1 YLJ2_CAEEL	P34367 caenorhabdi
13	39	62.9	420	1 SYS_MYCPN	P75107 mycoplasma
14	39	62.9	1209	1 LBN_BOVIN	Q8mi28 bos taurus
15	39	62.9	1220	1 LBN_MOUSE	Q8Klg2 mus musculu
16	39	62.9	1308	1 LBN_HUMAN	Q86uk5 homo sapien
17	38	61.3	116	1 VAM5_HUMAN	Q95183 homo sapien
18	38	61.3	349	1 TRUD_SALTI	Q8z473 salmonella
19	38	61.3	349	1 TRUD_SALTY	Q8zmf8 salmonella
20	38	61.3	357	1 CADH_POPDE	P31657 populus del
21	38	61.3	417	1 YC34_MYCPN	P75537 mycoplasma
22	38	61.3	512	1 VG29_BPMU	Q9t1w5 bacterioph
23	38	61.3	879	1 RA50_PYRHO	Q58687 pyrococcus
24	38	61.3	1935	1 MYSS_CYPCA	Q90339 cyprinus ca
25	38	61.3	1955	1 PUMA_PARUN	Q61308 halosarcis
26	37	59.7	460	1 SYS_HALMA	P54221 haloarcula
27	37	59.7	466	1 CYP8_CAEEL	P52016 caenorhabdi
28	37	59.7	617	1 UVRC_THETN	Q8r8m9 thermoanaer
29	37	59.7	635	1 DNAK_HALMA	Q01100 haloarcula
30	37	59.7	636	1 COS2_CARHY	Q9f8a8 carboxydoth
31	37	59.7	670	1 YDHK_ECO57	Q8x638 escherichia
32	37	59.7	670	1 YDHK_ECOLI	P76186 escherichia
33	37	59.7	687	1 WRK2_ARATH	Q9fg77 arabidopsis

34	37	59.7	721	1 DNAK_APHHA	O52960 aphanothece
35	37	59.7	775	1 CN04_MOUSE	Q8K3x4 mus musculu
36	37	59.7	796	1 CN04_HUMAN	Q9h1b7 homo sapien
37	37	59.7	868	1 CLP_TRYBB	P31543 trypanosoma
38	37	59.7	1191	1 SMC2_MOUSE	Q8cg48 mus musculu
39	36	58.1	76	1 KEC2_ECOLI	P13966 escherichia
40	36	58.1	209	1 YNU1_SHIFL	P29770 shigella fl
41	36	58.1	297	1 YJUP_HAEIN	P44520 haemophilus
42	36	58.1	338	1 TAP4_HUMAN	Q01664 homo sapien
43	36	58.1	402	1 OFS4_CANAL	P46596 candida alb
44	36	58.1	420	1 NCB2_HUMAN	P80303 homo sapien
45	36	58.1	448	1 VIME_CRIGR	P48670 cricetus

ALIGNMENTS

RESULT 1
SN25_HUMAN
ID SN25_HUMAN STANDARD; PRT; 206 AA.
AC P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN SNAP25 OR SNAP.
OS Homo sapiens (Human),
OS Macaca mulatta (Rhesus macaque),
OS Mus musculus (Mouse),
OS Rattus norvegicus (Rat), and
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 9544, 10090, 10116, 9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RC SPECIES=Human; TISSUE=Brain;
RX MEDLINE=94156217; PubMed=8112622;
RA Bark I.C., Wilson M.C.;
RT "Human cDNA clones encoding two different isoforms of the nerve terminal protein SNAP-25.";
RL Gene 139:291-292(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
RC SPECIES=Human; TISSUE=Brain;
RX MEDLINE=9433829; PubMed=8056350;
RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
RT "Cloning and sequence analysis of the human SNAP25 cDNA.";
RL Gene 145:313-314(1994).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC SPECIES=Human; TISSUE=Skeletal muscle;
RX MEDLINE=96332494; PubMed=8760387;
RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,
RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,
RA Frenkel M.J., Ward C.W.;
RT "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2.";
RL Biochem. J. 317:945-954(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaeslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RN Nature 414:865-871(2001).
 [5]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Human; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=M.mullatta; TISSUE=Hippocampus;
 RX Jensen M.J., Smith L.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [7]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=BALB/c;
 RX MEDLINE=90078337; PubMed=2592413;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 RA Bloom F.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein,
 RT SNAP-25, differentially expressed by neuronal subpopulations.";
 RL J. Cell Biol. 109:3039-3052(1989).
 [8]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=ILS, and ISS;
 RX MEDLINE=21363810; PubMed=11471062;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 RT "High-throughput sequence identification of gene coding variants
 RT within alcohol-related QTLs.";
 RL Mamm. Genome 12:657-663(2001).
 [9]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [10]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
 RA Strausberg R.L.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 [11]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Rat;
 RX Kataoka M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 [12]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Rat; TISSUE=Brain;
 RA Cho A.R., You K.H.;
 RT "Cloning of the SNAP-25 gene from a rat brain cDNA library.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [13]
 RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Rat; TISSUE=Brain;
 RX MEDLINE=99155074; PubMed=10037470;
 RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
 RT "SNARE complex proteins, including the cognate pair VAMP-2 and
 RT syntaxin-4, are expressed in cultured oligodendrocytes.";
 RL J. Neurochem. 72:988-998(1999).
 [14]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken; TISSUE=Retina;
 RX MEDLINE=91126080; PubMed=1992470;
 RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
 RA Wilson M.C.;
 RT "Expression of a conserved cell-type-specific protein in nerve
 RT terminals coincides with synaptogenesis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
 [15]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Chicken;
 RX MEDLINE=93389738; PubMed=8377193;
 RA Bark I.C.;
 RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
 RT encoding distinct isoforms of the protein.";
 RL J. Mol. Biol. 233:67-76(1993).
 [16]
 RP PALMITOYLATION.
 RC SPECIES=Rat;
 RX MEDLINE=93100552; PubMed=1281490;
 RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
 RT methionine-rich polypeptide in rapid axonal transport and a major

Query Match 100.0%; Score 62; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELEMQRADQLA 13
| | | | | | | | | | | | | | |
Db 10 ELEMQRADQLA 22

RESULT 2

SN2A_CARAU STANDARD; PRT; 204 AA.
AC P36977;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25A (SNAP-25A).
GN SNAP-A.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

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EMBL; L22973; AAA16537.1; -
PIR; I50480;
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; T SNARE; 2.
KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.
FT DOMAIN 19 81
FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 85 92 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 85 92 CYS-RICH.
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFCFC09189 CRC64;

Query Match 80.6%; Score 50; DB 1; Length 204;
Best Local Similarity 76.9%; Pred. No. 0.41;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELEMQRADQLA 13
| | | | | | | | | | | | | | |
Db 10 ELEMQRADQLA 22

RESULT 3

KF3A_MOUSE

ID AC P28741;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kinesin-like protein KIF3A (Microtubule plus end-directed kinesin motor 3A).
DE motor 3A).
GN KIF3A OR KIF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93077686; PubMed=1447303;
RA Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M., Hirokawa N.;
RT "Kinesin family in murine central nervous system";
RL J. Cell Biol. 119:1287-1296(1992).
CC -!- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING ACTIVITY IN VITRO.
CC -!- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
CC -!- TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN ADULT BRAIN TISSUE (MAINLY IN THE CEREBELLAR GRANULAR LAYER) WITHIN A SINGLE TYPE OF NEURONAL CELL.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.

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EMBL; D12645; BAA02166.1; -
PIR; B44259; B44259.
DR HSPP; P17119; 3KAR.
DR MGD; MGI:107689; Kif3a.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.
KW Motor protein; Microtubule; ATP-binding; Coiled coil; Neurone.
FT DOMAIN 1 350 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 351 598 COILED COIL (BY SIMILARITY).
FT DOMAIN 599 701 GLOBULAR.
FT NP_BIND 100 107 ATP (BY SIMILARITY).
FT DOMAIN 442 445 POLY-GLU.
FT DOMAIN 509 512 POLY-ARG.
SQ SEQUENCE 701 AA; 80167 MW; 2405872DF2D85A29 CRC64;

Query Match 71.0%; Score 44; DB 1; Length 701;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELEMQRADQL 12
| | | | | | | | | | | | | | |
Db 505 ELEERRRRRAEQL 516

RESULT 4

SN2B_CARAU STANDARD; PRT; 203 AA.
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25B (SNAP-25B).

GN SNAP-B.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, piriform cortex, anterior thalamic nuclei, pontine nuclei, and granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC
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CC
CC EMBL; L22976; AAA16538.1; -.
CC PIR; I50481; I50481.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC Pfam; PF00835; SNAP-25; 1.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS50192; T-SNARE; 2.
KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 85 92 CYS-RICH.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBDBED37D6D7 CRC64;
Query Match 69.4%; Score 43; DB 1; Length 203;
Best Local Similarity 75.0%; Pred. No. 5.3;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ELEEMQRRADQL 12
|| :|||
Db 10 ELTDMQARADQL 21
RESULT 5
SN25_TORMA STANDARD; PRT; 210 AA.
AC P36976;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25).
OS Torpedo marmorata (Marbled electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristiogaster; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7788;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Electric lobe;
RX MEDLINE=94043281; PubMed=8226991;
RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
RT "Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) shown by Drosophila and Torpedo cDNA clones."
RL J. Biol. Chem. 268:24408-24414(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC
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CC
CC EMBL; L22020; AAA49284.1; -.
CC PIR; I50552; I50552.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC Pfam; PF00835; SNAP-25; 1.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS50192; T-SNARE; 2.
KW Synaptosome; Neurone; Repeat; Coiled coil.
FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 88 96 CYS-RICH.
SQ SEQUENCE 210 AA; 23652 MW; 58FE471A9234B8B1 CRC64;
Query Match 67.7%; Score 42; DB 1; Length 210;
Best Local Similarity 75.0%; Pred. No. 7.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ELEEMQRRADQL 12
| | | | | | | | | |
Db 14 EQEEMQRCADQI 25
RESULT 6
PFDA_METKA STANDARD; PRT; 157 AA.
AC Q8TU77;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prefoldin alpha subunit (GimC alpha subunit).
GN PFDA OR MK1614.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -!- FUNCTION: Molecular chaperone capable of stabilizing a range of proteins. Seems to fulfil an ATP-independent, HSP70-like function in archaeal de novo protein folding (By similarity).

```

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)}.
RN [3]
RP SEQUENCE FROM N.A.
RA Connolly K.S., Gunning K.M., Davis C.A., Kadner K., Subramanian S.,
RA Miguel T., Lewis K.D., Fridlyand J., Alcivare D., Benke J.A.,
RA Bondoc M., Bowen E., Chiang A., Critz P., Jaklevic M.A., Lindo K.,
RA Lindquist K., Miller C., Patel S., Piscia C., Riley B.E., Rojeski H.,
RA Sarmiento R., Yu C., Montenegro M., Aerts A., Chung A., Abrajano A.,
RA Baker M., Gau C., Jett J., Ko C., Beall K., Woolley J.P., Stultz J.L.,
RA Kimmerly W., Martin C.H.;
RT "Sequencing of human chromosome 5.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBDJ databases.
CC -1- FUNCTION: MICROTUBULE-BASED ANTROGRADE TRANSLOCATOR FOR
CC MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING
CC ACTIVITY IN VITRO.
CC
CC -1- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
CC
CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC II SUBFAMILY.
CC
CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC
CC -----
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CC -----
DR EMBL; AF041853; AAC72294.1; -.
DR EMBL; BC045542; AAH45542.1; -.
DR EMBL; AC004237; AAC04475.1; ALT_SEQ.
DR HSSP; PI7119; 3KAR.
DR Genew; HGNC:6319; KIF3A.
DR MIM; 604683; -.
DR GO; GO:0006996; P:organelle organization and biogenesis; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
DR KW Motor protein; Microtubule; ATP-binding; Coiled coil; Neurone.
DR DOMAIN 1 350 KINESIN-MOTOR.
DR DOMAIN 351 599 COILED COIL (BY SIMILARITY).
DR DOMAIN 600 702 GLOBULAR.
DR NP_BIND 100 107 ATP (BY SIMILARITY).
DR DOMAIN 443 446 POLY-GLU.
DR CONFLICT 151 151 E -> G (IN REF. 2).
DR CONFLICT 170 170 E -> A (IN REF. 1).
DR CONFLICT 172 172 K -> I (IN REF. 2).
DR SQ SEQUENCE 702 AA; 80385 MW; 88E55D21209B4E14 CRC64;

Query Match 66.1%; Score 41; DB 1; Length 702;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMQRADQL 12
Db 506 ELEERRKAEQL 517
|||||:|:|:|

RESULT 8
VAM5 RAT
ID VAM5 RAT STANDARD; PRT; 102 AA.
AC Q9Z2J5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vesicle-associated membrane protein 5 (VAMP-5) (Myobrevin).
GN VAMP5.

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DE type B) (Nonmuscle myosin heavy chain-B) (NMHC-B).
GN MYH10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96025307; PubMed=7499478;
RA Phillips C.L., Yamakawa K., Adelstein R.S.;
RT "Cloning of the cDNA encoding human nonmuscle myosin heavy chain-B and
RT analysis of human tissues with isoform-specific antibodies.";
RL J. Muscle Res. Cell Motil. 16:379-389(1995).
RN [2]
RP SEQUENCE OF 63-722 FROM N.A.
RX MEDLINE=91316803; PubMed=1860190;
RA Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K.,
RA Gdula D., Adelstein R.S., Weir L.;
RT "Human nonmuscle myosin heavy chains are encoded by two genes located
RT on different chromosomes.";
RL Circ. Res. 69:530-539(1991).
CC -!- FUNCTION: Cellular myosin appears to play a role in cytokinesis,
CC cell shape, and specialized functions such as secretion and
CC capping.
CC -!- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy
CC chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2
CC regulatory light chain subunits (MLC-2).
CC -!- DOMAIN: The rodlike tail sequence is highly repetitive, showing
CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
CC characteristic for alpha-helical coiled coils.
CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -!- SIMILARITY: Contains 1 IQ domain.
CC -----
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CC -----
DR EMBL; M69181; AAA99177.1; -.
DR PIR; A59252; A59252.
DR HSSP; P10587; 1BR2.
DR Genew; HGNC:7568; MYH10.
DR MIM; 160776; -.
DR GO; GO:0016459; C:myosin; NAS.
DR GO; GO:0003779; F:actin binding; NAS.
DR GO; GO:0005524; F:ATP binding; NAS.
DR GO; GO:0000910; P:cytokinesis; NAS.
DR InterPro; IPR000048; IQ region.
DR InterPro; IPR001609; Myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS00096; IQ; 1.
DR Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil;
KW Multigene family.
FT DOMAIN 1 785 MYOSIN HEAD-LIKE.
FT DOMAIN 786 815 IQ.
FT DOMAIN 845 1976 COILED COIL (POTENTIAL).
FT NP BIND 178 185 ATP (POTENTIAL).
SQ SEQUENCE 1976 AA; 228938 MW; B2BB87FF35EA124F CRC64;
Query Match 64.5%; Score 40; DB 1; Length 1976;
```

```
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
Db 874 ELEMERKHQQL 885
|||||:|
|

RESULT 11
MYHA RAT
ID MYHA RAT STANDARD; PRT; 1976 AA.
AC Q9JUL70;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
DE type B) (Nonmuscle myosin heavy chain-B) (NMHC-B).
GN MYH10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=20483650; PubMed=11027611;
RA Yam J.W.P., Chan K.W., Li N., Hsiao W.L.W.;
RT "Molecular cloning and functional analysis of the promoter region of
RT rat nonmuscle myosin heavy chain-B gene.";
RL Biochem. Biophys. Res. Commun. 276:1203-1209(2000).
CC -!- FUNCTION: Cellular myosin appears to play a role in cytokinesis,
CC cell shape, and specialized functions such as secretion and
CC capping.
CC -!- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy
CC chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2
CC regulatory light chain subunits (MLC-2).
CC -!- DOMAIN: The rodlike tail sequence is highly repetitive, showing
CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
CC characteristic for alpha-helical coiled coils.
CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -!- SIMILARITY: Contains 1 IQ domain.
CC -----
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CC -----
DR EMBL; AF139055; AAF61445.1; -.
DR HSSP; P10587; 1BR2.
DR InterPro; IPR000048; IQ region.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS00096; IQ; 1.
DR Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil;
KW Multigene family.
FT DOMAIN 1 785 MYOSIN HEAD-LIKE.
FT DOMAIN 786 815 IQ.
FT DOMAIN 845 1976 COILED COIL (POTENTIAL).
FT NP BIND 178 185 ATP (POTENTIAL).
SQ SEQUENCE 1976 AA; 228963 MW; E32708BF9BF2B470 CRC64;
```

Query Match 64.5%; Score 40; DB 1; Length 1976;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
Db 874 ELEMORRADQL 885

RESULT 12

YLJ2 CAEEL STANDARD; PRT; 2107 AA.
AC P34367; Q18736;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein C50C3.2 in chromosome III.
GN C50C3.2/C50C3.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the spectrin family.
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CC
DR EMBL; L14433; AAA27974.2; -.
DR WormPep; C50C3.2; CE01861.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00435; spectrin; 6.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EPH; 2.
DR SMART; SM00150; SPC; 6.
DR PROSITE; PS00018; EF_HAND; 1.
KW Hypothetical protein; Calcium-binding; Repeat.
FT CA BIND 2025 2036 EF-HAND (POTENTIAL).
SQ SEQUENCE 2107 AA; 246123 MW; B5C3C51EC0EDA2E9 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 2107;
Best Local Similarity 53.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 13
Db 1272 DIERNQKRHDELA 1284

RESULT 13

SYS MYCPN STANDARD; PRT; 420 AA.
AC P75107;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (serRS).
GN SERS OR MPN005 OR MP149.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP + diphosphate
+ L-seryl-tRNA(Ser).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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CC
DR EMBL; AE000016; AAB95797.1; -.
DR PIR; S73475; S73475.
DR HSSP; P34945; 1SER.
DR HAMAP; MF_00176; -; 1.
DR InterPro; IPR002314; tRNA-synt 2b.
DR InterPro; IPR002317; tRNA-synt_ser.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF02403; Seryl_tRNA_N; 1.
DR Pfam; PF00587; tRNA-synt 2b; 1.
DR PRINTS; PR00981; TRNASYNTHSER.
DR TIGRFAMS; TIGR00414; serS; 1.
DR PROSITE; PS50862; AA TRNA_LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 420 AA; 47924 MW; 9BC071823D20998E CRC64;

Query Match 62.9%; Score 39; DB 1; Length 420;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
Db 292 ELEMTRDAEQI 303

RESULT 14

LBV BOVIN STANDARD; PRT; 1209 AA.
AC Q8MT28;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Limbin.

GN EVC2 OR LBN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND DISEASE.
RC TISSUE=Bone;
RX MEDLINE=22155879; PubMed=12136126;
RA Takeda H., Takami M., Oguni T., Tsuji T., Yoneda K., Sato H.,
RA Ihara N., Itoh T., Kata S.R., Mishina Y., Womack J.E., Moritomo Y.,
RA Sugimoto Y., Kunieda T.;
RT "Positional cloning of the gene LIMBIN responsible for bovine
RT chondrodysplastic dwarfism.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10549-10554(2002).
CC -!- FUNCTION: Plays a critical role in bone formation and skeletal
CC development.
CC -!- DISEASE: Defects in EVC2 are the cause of bovine chondrodysplastic
CC dwarfism (BCD). BCD is an autosomal recessive disorder
CC characterized by short limbs, joint abnormalities and ateliosis.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB083065; BAC06588.1; --
DR Transmembrane; Coiled coil; Dwarfism.
FT TRANSMEM 201 221 POTENTIAL.
FT DOMAIN 355 394 COILED COIL (POTENTIAL).
FT DOMAIN 553 697 COILED COIL (POTENTIAL).
FT DOMAIN 920 1012 COILED COIL (POTENTIAL).
SQ SEQUENCE 1209 AA; 137811 MW; D78106F1001785AB CRC64;

Query Match 62.9%; Score 39; DB 1; Length 1209;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEEMQRRADQLA 13
|||:|||||
Db 621 LEELQERLDQAA 632

RESULT 15
LBN MOUSE
ID LBN_MOUSE STANDARD; PRT; 1220 AA.
AC Q8KIG2; Q8BRF3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Limbin.
GN EVC2 OR LBN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Limb bud;
RX MEDLINE=22155879; PubMed=12136126;
RA Takeda H., Takami M., Oguni T., Tsuji T., Yoneda K., Sato H.,
RA Ihara N., Itoh T., Kata S.R., Mishina Y., Womack J.E., Moritomo Y.,
RA Sugimoto Y., Kunieda T.;
RT "Positional cloning of the gene limbin responsible for bovine
RT chondrodysplastic dwarfism.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10549-10554(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 21-744 FROM N.A.
RC STRAIN=CS7BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Plays a critical role in bone formation and skeletal
CC development. May be involved in early embryonic morphogenesis.
CC -!- TISSUE SPECIFICITY: Expressed in long and cranial bones, kidney
CC and heart. Strongly expressed in proliferating chondrocytes,
CC osteoblasts and osteoclasts.
CC -!- DEVELOPMENTAL STAGE: Found in the embryo at day E7, E11, E15, and
CC E17. At the limb bud formation stage E11, it is expressed in fore-
CC and hindlimb buds, branchial arches, and facial primordia.
CC
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CC
CC EMBL; AB083066; BAC06589.1; --
DR EMBL; BC037473; AAH37473.1; --

DR EMBL; AK044977; BAC32167.1; ALT_INIT.
DR MGD; MGI:1915775; Evc2.
KW Transmembrane; Coiled coil.
FT TRANSMEM 211 231 POTENTIAL.
FT DOMAIN 355 404 COILED COIL (POTENTIAL).
FT DOMAIN 563 644 COILED COIL (POTENTIAL).
FT DOMAIN 854 875 COILED COIL (POTENTIAL).
FT DOMAIN 920 1005 COILED COIL (POTENTIAL).
SQ SEQUENCE 1220 AA; 137638 MW; E67671714A866B1D CRC64;
Query Match 62.9%; Score 39; DB 1; Length 1220;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 LEMQRRADQLA 13
Db 631 LEEQLERLDQAA 642

Search completed: March 4, 2004, 08:25:56
Job time : 15.3684 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 17.7895 Seconds
(without alignments)
70.294 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEMORRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	206	2 A37861	synaptosomal-assoc
2	62	100.0	206	2 I53735	nerve terminal pro
3	62	100.0	206	2 I67823	nerve terminal pro
4	62	100.0	206	2 A33623	synaptosomal-assoc
5	62	100.0	249	2 S38308	SNAP-25 protein -
6	62	100.0	249	2 S38309	SNAP-25 protein -
7	57	91.9	56	2 S36812	probable synapse-a
8	50	80.6	204	2 I50480	synapse protein SN
9	44	71.0	701	1 B44259	kinesin-related pr
10	43	69.4	203	2 I50481	synapse protein SN
11	42	67.7	210	2 I50552	synapse protein -
12	41	66.1	480	2 D75050	hypothetical prote
13	41	66.1	664	2 D84374	hypothetical prote
14	40	64.5	149	2 AB1645	Portein gp28 (Bact
15	40	64.5	924	2 S06117	myosin heavy chain
16	40	64.5	1009	2 S44621	C50C3.2 protein -
17	40	64.5	1976	2 A59252	myosin heavy chain
18	40	64.5	1999	1 S21801	myosin heavy chain
19	40	64.5	2007	1 B43402	myosin heavy chain
20	39	62.9	119	2 E98090	hypothetical prote
21	39	62.9	190	2 G82840	hypothetical prote
22	39	62.9	420	2 S73475	serine-tRNA ligase
23	39	62.9	532	2 G87912	protein B0205.9 [i
24	38	61.3	91	2 B75601	hypothetical prote
25	38	61.3	136	2 D70361	transcriptional regu
26	38	61.3	266	2 A12283	hypothetical prote
27	38	61.3	294	2 S75135	hypothetical prote
28	38	61.3	341	2 S31571	cinnamyl-alcohol d
29	38	61.3	349	2 AC0856	conserved hypothet

30	38	61.3	357	2 T09141	cinnamyl-alcohol d
31	38	61.3	417	2 S73923	MG288 homolog G07
32	38	61.3	500	2 A82497	ribose ABC transpo
33	38	61.3	702	2 T16401	alpha-1,3-mannosyl
34	38	61.3	879	2 C71083	conserved hypothet
35	38	61.3	920	2 AD2143	two-component sens
36	38	61.3	1210	2 H88451	protein ZC155.3 [i
37	38	61.3	1955	2 T30934	myosin-like protei
38	37	59.7	283	2 S42393	G-box-binding prot
39	37	59.7	309	2 E69200	conserved hypothet
40	37	59.7	460	2 T47108	serine-tRNA ligase
41	37	59.7	466	2 T18575	cyclophilin isofor
42	37	59.7	470	2 AC0049	hypothetical prote
43	37	59.7	474	2 F87152	fumarate [imported
44	37	59.7	506	2 AH0509	citrate (pro-3S)-l
45	37	59.7	609	2 T28896	hypothetical prote

ALIGNMENTS

RESULT 1

A37861
synaptosomal-associated 25K protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
R;Accession: A37861
R;Catsicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A;Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid
A;Reference number: A37861; MUID:91126080; PMID:1992470
A;Accession: A37861
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAT>
A;Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
| | | | | | | | | | | | | |
Db 10 ELEMORRADQLA 22

RESULT 2

I53735
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
R;Accession: I53735
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal proteir
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I53735
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: GB:L19760; NID:g307425; PIDN:AAC37545.1; PID:g307426
C;Genetics:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
| | | | | | | | | | | | | |
Db 10 ELEMORRADQLA 22

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RESULT 3
I67823
nerve terminal protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C;Accession: I67823
R;Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A;Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A;Reference number: I53735; MUID:94156217; PMID:8112622
A;Accession: I67823
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: GB:I19761; NID:g307427; PIDN:AAC37546.1; PID:g307428
C;Genetics:
A;Gene: GDB:SNAP
A;Cross-references: GDB:355671; OMIM:600322
A;Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||||
Db 10 ELEMORRADQLA 22

RESULT 4
A33623
synaptosomal-associated 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C;Accession: A33623
R;Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.;
J. Cell Biol. 109, 3039-3052, 1989
A;Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differ
A;Reference number: A33623; MUID:90078337; PMID:2592413
A;Accession: A33623
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <OYL>
A;Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AA61741.1; PID:g200998

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||||
Db 10 ELEMORRADQLA 22

RESULT 5
S38308
SNAP-25 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S38308
R;Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A;Reference number: S38308; MUID:93389738; PMID:8377193
A;Accession: S38308
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <BAR>
A;Cross-references: EMBL:L09250
C;Genetics:
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||||
Db 10 ELEMORRADQLA 22

RESULT 6
S38309
SNAP-25 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S38309
R;Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A;Reference number: S38308; MUID:93389738; PMID:8377193
A;Accession: S38309
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <BAR>
A;Cross-references: EMBL:L09250
C;Genetics:
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||||
Db 10 ELEMORRADQLA 22

RESULT 7
S36812
probable synapse-associated 28K protein - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: S36812
R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A;Reference number: S36811; MUID:93374072; PMID:8365494
A;Accession: S36812
A;Molecule type: protein
A;Residues: 1-56 <HOR>
A;Experimental source: brain

Query Match 91.9%; Score 57; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEEMORRADQLA 13
|||||
Db 1 LEEMORRADQLA 12

RESULT 8
I50480
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50480
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94069448; PMID:8248151
A;Accession: I50480
A;Status: preliminary; translated from GB/EMBL/DBJ
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Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||||
Db 10 ELEMORRADQLA 22

RESULT 6
S38309
SNAP-25 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S38309
R;Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A;Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A;Reference number: S38308; MUID:93389738; PMID:8377193
A;Accession: S38309
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <BAR>
A;Cross-references: EMBL:L09250
C;Genetics:
A;Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||||
Db 10 ELEMORRADQLA 22

RESULT 7
S36812
probable synapse-associated 28K protein - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: S36812
R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A;Reference number: S36811; MUID:93374072; PMID:8365494
A;Accession: S36812
A;Molecule type: protein
A;Residues: 1-56 <HOR>
A;Experimental source: brain

Query Match 91.9%; Score 57; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEEMORRADQLA 13
|||||
Db 1 LEEMORRADQLA 12

RESULT 8
I50480
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50480
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94069448; PMID:8248151
A;Accession: I50480
A;Status: preliminary; translated from GB/EMBL/DBJ
```

A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Cross-references: GB:L22973; NID:g349426; PIDN:AAA16537.1; PID:g349427
C;Genetics:
A;Gene: SNAP-25

Query Match 80.6%; Score 50; DB 2; Length 204;
Best Local Similarity 76.9%; Pred. No. 0.73;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||:|||||
Db 10 ELSDMQQRADQLA 22
|||:|||||

RESULT 9
B44259
kinesin-related protein KIF3A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
C;Accession: B44259; S27872
R;Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous system.
A;Reference number: A44259; MUID:93077686; PMID:1447303
A;Accession: B44259
A;Molecule type: mRNA
A;Residues: 1-701 <AIZ>
A;Cross-references: EMBL:D12645; NID:g220469; PIDN:BAA021166.1; PID:g220470
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118911)
C;Complex: heterodimer with KIF3B (PIR:A57107); the KIF3A/3B heterodimer associates with C;Function:
A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal transport.
C;Superfamily: Kinesin-related protein KIF3; kinesin motor domain homology
C;Keywords: ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; nucleotide F;1-368/Domain: head globular #status predicted <HGL>
F;15-351/Domain: kinesin motor domain homology <KMT>
F;100-107/Region: nucleotide-binding motif A (P-loop)
F;369-599/Domain: helical rod #status predicted <ROD>
F;600-701/Domain: tail globular #status predicted <TGL>
F;106/Binding site: ATP (Lys) #status predicted

Query Match 71.0%; Score 44; DB 1; Length 701;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
||||:|||||
Db 505 ELEERRRAEQL 516
||||:|||||

RESULT 10
I50481
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50481
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: GB:L22976; NID:g349430; PIDN:AAA16538.1; PID:g349431
C;Genetics:
A;Gene: SNAP-25

Query Match 69.4%; Score 43; DB 2; Length 203;
Best Local Similarity 75.0%; Pred. No. 9.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Cross-references: GB:L22973; NID:g349426; PIDN:AAA16537.1; PID:g349427
C;Genetics:
A;Gene: SNAP-25

Query Match 80.6%; Score 50; DB 2; Length 204;
Best Local Similarity 76.9%; Pred. No. 0.73;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||:|||||
Db 10 ELSDMQQRADQLA 22
|||:|||||

RESULT 9
B44259
kinesin-related protein KIF3A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
C;Accession: B44259; S27872
R;Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous system.
A;Reference number: A44259; MUID:93077686; PMID:1447303
A;Accession: B44259
A;Molecule type: mRNA
A;Residues: 1-701 <AIZ>
A;Cross-references: EMBL:D12645; NID:g220469; PIDN:BAA021166.1; PID:g220470
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118911)
C;Complex: heterodimer with KIF3B (PIR:A57107); the KIF3A/3B heterodimer associates with C;Function:
A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal transport.
C;Superfamily: Kinesin-related protein KIF3; kinesin motor domain homology
C;Keywords: ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; nucleotide F;1-368/Domain: head globular #status predicted <HGL>
F;15-351/Domain: kinesin motor domain homology <KMT>
F;100-107/Region: nucleotide-binding motif A (P-loop)
F;369-599/Domain: helical rod #status predicted <ROD>
F;600-701/Domain: tail globular #status predicted <TGL>
F;106/Binding site: ATP (Lys) #status predicted

Query Match 71.0%; Score 44; DB 1; Length 701;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
||||:|||||
Db 505 ELEERRRAEQL 516
||||:|||||

RESULT 10
I50481
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50481
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: GB:L22976; NID:g349430; PIDN:AAA16538.1; PID:g349431
C;Genetics:
A;Gene: SNAP-25

Query Match 69.4%; Score 43; DB 2; Length 203;
Best Local Similarity 75.0%; Pred. No. 9.6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
|||:|||||
Db 10 ELTDMQARADQL 21
|||:|||||

RESULT 11
I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50552
R;Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone, V.
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) sh
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: GB:L22020; NID:g431296; PIDN:AAA49284.1; PID:g431297

Query Match 67.7%; Score 42; DB 2; Length 210;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
|||:|||||
Db 14 EQEEMQRCADQI 25
|||:|||||

RESULT 12
D75050
hypothetical protein PAB1455 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
C;Accession: D75050
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: D75050
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <KAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50297.1; PID:g545881
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1455
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1455

Query Match 66.1%; Score 41; DB 2; Length 480;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
|||:|||||
Db 150 ELEEAKRRAEEL 161
|||:|||||

RESULT 13
D84374
hypothetical protein Vng2238c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84374
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: D84374
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-664 <STO>
 A;Cross-references: GB:AE004437; NID:G10581651; PIDN:AG20360.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: VNG2238C

Query Match 66.1%; Score 41; DB 2; Length 664;
 Best Local Similarity 66.7%; Pred. No. 65;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
 ||||: |||:
 Db 494 EEEQERADEL 505

RESULT 14
 AB1645
 Portein gp28 (Bacteriophage A118) [imported] - Listeria innocua (strain Clip11262)
 C;Species: Listeria innocua
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C;Accession: AB1645
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AB1645
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-149 <GLA>
 A;Cross-references: GB:AL592022; PIDN:CAC96930.1; PID:G16414186; GSPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin1699

Query Match 64.5%; Score 40; DB 2; Length 149;
 Best Local Similarity 53.8%; Pred. No. 21;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
 ||||: |||:
 Db 64 ELEDLEKNADDLA 76

RESULT 15
 S06117
 myosin heavy chain, nonmuscle (clone lambda-FMHC) - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Jun-2000
 C;Accession: S06117
 R;Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
 Eur. J. Biochem. 184, 611-616, 1989
 A;Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in
 s.
 A;Reference number: S06116; MUID:90032648; PMID:2806244
 A;Accession: S06117
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-924 <KAT>
 A;Cross-references: GB:X17590
 A;Note: this translation is not annotated in GenBank entry GGMHCFC, release 114
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 F;1-303/Domain: myosin motor domain homology (fragment) <MMOT>

Query Match 64.5%; Score 40; DB 2; Length 924;
 Best Local Similarity 66.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
 ||||: |||:
 Db 406 ELEMQRKHQQL 417

Search completed: March 4, 2004, 08:29:54
 Job time : 18.7895 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:20 ; Search time 37.6316 Seconds
(without alignments)
72.944 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEMORRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	206	10	US-09-942-024-2
2	62	100.0	206	10	US-09-942-024-7
3	62	100.0	206	10	US-09-942-024-12
4	62	100.0	206	10	US-09-942-098-2
5	62	100.0	206	10	US-09-942-098-7
6	62	100.0	206	10	US-09-942-098-12
7	62	100.0	249	10	US-09-942-024-16
8	62	100.0	249	10	US-09-942-098-16
9	43	69.4	203	10	US-09-942-024-14
10	43	69.4	203	10	US-09-942-098-14
11	40	64.5	312	10	US-09-976-782-32
12	40	64.5	312	15	US-10-080-334-167
13	40	64.5	312	15	US-10-080-334-188
14	40	64.5	312	15	US-10-080-334-270
15	40	64.5	312	15	US-10-231-913-260

16	40	64.5	1009	15	US-10-369-493-5795	Sequence 5795, Ap
17	40	64.5	1999	15	US-10-028-248A-107	Sequence 107, App
18	40	64.5	1999	15	US-10-107-782-107	Sequence 107, App
19	39	62.9	442	14	US-10-241-220-110	Sequence 110, App
20	38	61.3	102	9	US-09-745-763-6	Sequence 6, Appli
21	38	61.3	116	14	US-10-308-279-68	Sequence 68, Appli
22	38	61.3	116	14	US-10-357-028-4	Sequence 4, Appli
23	38	61.3	116	15	US-10-264-237-1808	Sequence 1808, Ap
24	38	61.3	173	9	US-09-272-809-16	Sequence 16, Appli
25	38	61.3	357	9	US-09-947-027-9	Sequence 9, Appli
26	38	61.3	357	13	US-10-091-009-9	Sequence 9, Appli
27	38	61.3	870	14	US-10-156-761-12048	Sequence 12048, A
28	38	61.3	879	15	US-10-369-493-1271	Sequence 1271, Ap
29	38	61.3	879	15	US-10-369-493-20337	Sequence 20337, A
30	37	59.7	70	14	US-10-078-090-161	Sequence 161, App
31	37	59.7	229	15	US-10-374-780A-1453	Sequence 1453, Ap
32	37	59.7	324	15	US-10-369-493-8329	Sequence 8329, Ap
33	37	59.7	687	10	US-09-934-455-18	Sequence 18, Appli
34	37	59.7	687	14	US-10-295-403-76	Sequence 76, Appli
35	37	59.7	687	15	US-10-374-780A-174	Sequence 174, App
36	37	59.7	723	13	US-10-044-205A-32	Sequence 32, Appli
37	37	59.7	796	13	US-10-044-205A-31	Sequence 31, Appli
38	37	59.7	851	14	US-10-156-761-9933	Sequence 9933, Ap
39	36	58.1	21	14	US-10-113-424-96	Sequence 96, Appli
40	36	58.1	25	14	US-10-360-053-27	Sequence 27, Appli
41	36	58.1	57	9	US-09-864-761-41864	Sequence 41864, A
42	36	58.1	176	15	US-10-264-049-4068	Sequence 4068, Ap
43	36	58.1	244	15	US-10-369-493-2951	Sequence 2951, Ap
44	36	58.1	256	15	US-10-369-493-19362	Sequence 19362, A
45	36	58.1	295	15	US-10-369-493-18283	Sequence 18283, A

ALIGNMENTS

RESULT 1
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942, 024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
|||
Db 10 ELEMORRADQLA 22

RESULT 2
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger


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; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-942-024-7

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Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ELEEMQRRADQLA 13
| | | | | | | | | | | | | | | | | | | | | |
Db 10 ELEEMQRRADQLA 22

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RESULT 3
US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-942-024-12

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```

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ELEEMQRRADQLA 13
| | | | | | | | | | | | | | | | | | | | | |
Db 10 ELEEMQRRADQLA 22

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RESULT 4
US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-942-098-2

```

```

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ELEEMQRRADQLA 13
| | | | | | | | | | | | | | | | | | | | | |
Db 10 ELEEMQRRADQLA 22

```

```

RESULT 5
US-09-942-098-7
; Sequence 7, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-942-098-7

```

```

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ELEEMQRRADQLA 13
| | | | | | | | | | | | | | | | | | | | | |
Db 10 ELEEMQRRADQLA 22

```

```

RESULT 6
US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-942-098-12

```

```

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ELEEMQRRADQLA 13
| | | | | | | | | | | | | | | | | | | | | |
Db 10 ELEEMQRRADQLA 22

```

```

RESULT 7
US-09-942-024-16
; Sequence 16, Application US/09942024
; Publication No. US20030143650A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-024-16
```

```
Query Match 100.0%; Score 62; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ELEEMQRRADQLA 13
||| ||||| ||||| |||||
Db 10 ELEEMQRRADQLA 22
```

RESULT 8

```
US-09-942-098-16
; Sequence 16, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-098-16
```

```
Query Match 100.0%; Score 62; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ELEEMQRRADQLA 13
||| ||||| ||||| |||||
Db 10 ELEEMQRRADQLA 22
```

RESULT 9

```
US-09-942-024-14
; Sequence 14, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
```

```
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-14
```

```
Query Match 69.4%; Score 43; DB 10; Length 203;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 ELEEMQRRADQL 12
|| : || |||||
Db 10 ELTDMQARADQL 21
```

RESULT 10

```
US-09-942-098-14
; Sequence 14, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-14
```

```
Query Match 69.4%; Score 43; DB 10; Length 203;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 ELEEMQRRADQL 12
|| : || |||||
Db 10 ELTDMQARADQL 21
```

RESULT 11

```
US-09-976-782-32
; Sequence 32, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
```

; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 32
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Consensus
 ; OTHER INFORMATION: sequence
 US-09-976-782-32

Query Match 64.5%; Score 40; DB 10; Length 312;
 Best Local Similarity 58.3%; Pred. No. 75;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMQRRADQL 12
 |:|:|:|:|
 Db 55 EIEELRRQIDQL 66

RESULT 12

US-10-080-334-167
 ; Sequence 167, Application US/10080334
 ; Publication No. US20040002584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Li, Li
 ; APPLICANT: Shenoy, Suresh G
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Vernet, Corine A. M.
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gusev, Vladimir Y
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Boldog, Ferenc L
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Gangolli, Esha A
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Baumgartner, Jason C.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Spaderna, Steven K
 ; APPLICANT: Zerhusen, Bryan D
 ; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
 ; TITLE OF INVENTION: Using the Same
 ; FILE REFERENCE: 21402-275
 ; CURRENT APPLICATION NUMBER: US/10/080,334
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: 60/270,523
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/322,712
 ; PRIOR FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: 60/311,980
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: 60/330,307
 ; PRIOR FILING DATE: 2001-10-18
 ; PRIOR APPLICATION NUMBER: 60/278,796
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/281,521
 ; PRIOR FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: 60/276,677
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/311,595
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/270,220
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/274,295
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 60/318,526

; PRIOR FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 60/286,548
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 60/291,765
 ; PRIOR FILING DATE: 2001-05-17
 ; PRIOR APPLICATION NUMBER: 60/270,797
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: 60/276,400
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/270,810
 ; PRIOR FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 388
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 167
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-080-334-167

Query Match 64.5%; Score 40; DB 15; Length 312;
 Best Local Similarity 58.3%; Pred. No. 75;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMQRRADQL 12
 |:|:|:|:|
 Db 55 EIEELRRQIDQL 66

RESULT 13

US-10-080-334-188
 ; Sequence 188, Application US/10080334
 ; Publication No. US20040002584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Li, Li
 ; APPLICANT: Shenoy, Suresh G
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Vernet, Corine A. M.
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gusev, Vladimir Y
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Boldog, Ferenc L
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Gangolli, Esha A
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Baumgartner, Jason C.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Spaderna, Steven K
 ; APPLICANT: Zerhusen, Bryan D
 ; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
 ; TITLE OF INVENTION: Using the Same
 ; FILE REFERENCE: 21402-275
 ; CURRENT APPLICATION NUMBER: US/10/080,334
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: 60/270,523
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/322,712
 ; PRIOR FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: 60/311,980
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: 60/330,307
 ; PRIOR FILING DATE: 2001-10-18
 ; PRIOR APPLICATION NUMBER: 60/278,796
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/281,521
 ; PRIOR FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: 60/276,677
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/311,595
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/270,220
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/274,295
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 60/318,526

```

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 188
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-188

```

```

Query Match      64.5%; Score 40; DB 15; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 ELEMORRADQL 12
|:|:|:|:|
Db      55 EIEELRRQIDQL 66

```

```

RESULT 14
US-10-080-334-270
; Sequence 270, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980

```

```

; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 270
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-270

```

```

Query Match      64.5%; Score 40; DB 15; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 ELEMORRADQL 12
|:|:|:|:|
Db      55 EIEELRRQIDQL 66

```

```

RESULT 15
US-10-231-913-260
; Sequence 260, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

```

```
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 260
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-260
```

```
Query Match 64.5%; Score 40; DB 15; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 ELEEMORRADQL 12
|:|:|:|:|
Db 55 EIEELRRQIDQL 66
```

Search completed: March 4, 2004, 08:30:59
Job time : 37.6316 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:26:00 ; Search time 21.8947 Seconds
(without alignments)
30.653 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEMQRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	62	100.0	68	4	US-09-621-976-7614	Sequence 7614, Ap
2	62	100.0	206	1	US-08-393-985-18	Sequence 18, Appl
3	62	100.0	206	3	US-08-819-286-1	Sequence 1, Appli
4	40	64.5	415	4	US-09-252-991A-30511	Sequence 30511, A
5	38	61.3	116	3	US-08-621-018B-4	Sequence 4, Appli
6	38	61.3	116	4	US-09-483-665-4	Sequence 4, Appli
7	38	61.3	509	4	US-09-252-991A-23182	Sequence 23182, A
8	38	61.3	639	2	US-08-557-309B-37	Sequence 37, Appl
9	38	61.3	639	3	US-08-834-306-37	Sequence 37, Appl
10	38	61.3	639	3	US-08-993-674A-37	Sequence 37, Appl
11	38	61.3	639	4	US-09-256-976-37	Sequence 37, Appl
12	38	61.3	931	4	US-09-252-991A-22550	Sequence 22550, A
13	37	59.7	513	4	US-09-489-039A-13840	Sequence 13840, A
14	36	58.1	21	4	US-09-229-007A-96	Sequence 96, Appl
15	36	58.1	171	4	US-09-252-991A-24357	Sequence 24357, A
16	36	58.1	418	4	US-09-252-991A-20913	Sequence 20913, A
17	36	58.1	466	4	US-09-610-401-3	Sequence 3, Appli
18	36	58.1	466	4	US-09-610-401-4	Sequence 4, Appli
19	36	58.1	466	4	US-09-167-206-12	Sequence 12, Appl
20	36	58.1	514	4	US-09-107-532A-6282	Sequence 6282, Ap
21	36	58.1	567	4	US-09-489-039A-10840	Sequence 10840, A
22	36	58.1	823	4	US-09-252-991A-21027	Sequence 21027, A
23	36	58.1	1441	4	US-09-252-991A-28143	Sequence 28143, A
24	35	56.5	29	4	US-08-894-139-14	Sequence 14, Appl
25	35	56.5	102	3	US-09-383-586-34	Sequence 34, Appl
26	35	56.5	112	3	US-08-857-076-75	Sequence 75, Appl
27	35	56.5	147	3	US-09-383-586-35	Sequence 35, Appl

28	35	56.5	237	4	US-09-252-991A-19408	Sequence 19408, A
29	35	56.5	299	4	US-09-134-001C-4167	Sequence 4167, Ap
30	35	56.5	322	4	US-09-107-532A-6135	Sequence 6135, Ap
31	35	56.5	340	1	US-08-190-802A-42	Sequence 42, Appl
32	35	56.5	340	3	US-08-477-346-42	Sequence 42, Appl
33	35	56.5	340	4	US-08-473-089-42	Sequence 42, Appl
34	35	56.5	340	4	US-08-487-072A-42	Sequence 42, Appl
35	35	56.5	413	2	US-08-481-814A-8	Sequence 8, Appli
36	35	56.5	413	3	US-08-836-582-2	Sequence 2, Appli
37	35	56.5	413	4	US-09-265-566-2	Sequence 2, Appli
38	35	56.5	413	4	US-09-242-737-4	Sequence 4, Appli
39	35	56.5	494	4	US-09-489-039A-10240	Sequence 10240, A
40	35	56.5	570	3	US-09-135-020-114	Sequence 114, App
41	35	56.5	570	3	US-09-135-010A-114	Sequence 114, App
42	35	56.5	570	4	US-09-444-871-114	Sequence 114, App
43	35	56.5	570	4	US-09-597-735-114	Sequence 114, App
44	35	56.5	570	4	US-09-444-295-114	Sequence 114, App
45	35	56.5	570	4	US-09-597-732-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-09-621-976-7614
; Sequence 7614, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7614
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7614

Query Match 100.0%; Score 62; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
| | | | | | | | | | | | | |
Db 10 ELEMQRADQLA 22

RESULT 2
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-393-985-18

Query Match 100.0%; Score 62; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEEMQRRADQLA 13
   |||||
Db 10 ELEEMQRRADQLA 22

RESULT 3
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-1

Query Match 100.0%; Score 62; DB 3; Length 206;

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Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEEMQRRADQLA 13
   |||||
Db 10 ELEEMQRRADQLA 22

RESULT 4
US-09-252-991A-30511
; Sequence 30511, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30511
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-30511

Query Match 64.5%; Score 40; DB 4; Length 415;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEEEMQRRADQLA 13
   :|||
Db 65 VEEQRRVDHLA 76

RESULT 5
US-08-621-018B-4
; Sequence 4, Application US/08621018B
; Patent No. 6060239
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,018B
; FILING DATE: March 22, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0029-1 CIP
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: LUNGN0T01
CLONE: 122826
US-08-621-018B-4

Query Match 61.3%; Score 38; DB 3; Length 116;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
:|:|:|:|
Db 33 KLAELQQRSDQL 44

RESULT 6

US-09-483-665-4
Sequence 4, Application US/09483665
Patent No. 6534275
GENERAL INFORMATION:

APPLICANT: Stuart, Susan G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/483,665
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,018
FILING DATE: March 22, 1996
APPLICATION NUMBER: 08/409,373
FILING DATE: March 23, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-Cox, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-849-8886

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: LUNGN0T01
CLONE: 122826

US-09-483-665-4

Query Match 61.3%; Score 38; DB 4; Length 116;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
:|:|:|:|
Db 33 KLAELQQRSDQL 44

RESULT 7

US-09-252-991A-23182
Sequence 23182, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23182

LENGTH: 509
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23182

Query Match 61.3%; Score 38; DB 4; Length 509;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
:|:|:|:|
Db 349 ELEECQKAEEL 360

RESULT 8

US-08-557-309B-37
Sequence 37, Application US/08557309B
Patent No. 5916572
GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

```
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-557-309B-37

Query Match 61.3%; Score 38; DB 2; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EEMORRADQLA 13
Db 367 EEMIRRAEELA 377

RESULT 9
US-08-834-306-37
; Sequence 37, Application US/08834306
; Patent No. 6054135
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,306
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.422C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-834-306-37

Query Match 61.3%; Score 38; DB 3; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EEMORRADQLA 13
Db 367 EEMIRRAEELA 377

RESULT 10
US-08-993-674A-37
; Sequence 37, Application US/08993674A
; Patent No. 6228372
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; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Smith, John M.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,674A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.422C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-993-674A-37

Query Match 61.3%; Score 38; DB 3; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EEMORRADQLA 13
Db 367 EEMIRRAEELA 377

RESULT 11
US-09-256-976-37
; Sequence 37, Application US/09256976
; Patent No. 6419933
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Smith, John M.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
; TITLE OF INVENTION: OF T. CRUZI INFECTION
; FILE REFERENCE: 210121.422C3
; CURRENT APPLICATION NUMBER: US/09/256,976
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
; FEATURE:
; OTHER INFORMATION: Where any Xaa is an independently selected amino
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; OTHER INFORMATION: acid
US-09-256-976-37

Query Match 61.3%; Score 38; DB 4; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEMQRRADQLA 13
||| |||: ||
Db 367 EEMIRAEELA 377

RESULT 12

US-09-252-991A-22550
; Sequence 22550, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22550
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22550

Query Match 61.3%; Score 38; DB 4; Length 931;
Best Local Similarity 63.6%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQ 11
::|| ||: ||
Db 601 QVEERQADQ 611

RESULT 13

US-09-489-039A-13840
; Sequence 13840, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13840
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13840

Query Match 59.7%; Score 37; DB 4; Length 513;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEMQRRADQLA 13
| |||: ||
Db 101 LEMQRRADQAA 112

RESULT 14

US-09-229-007A-96
; Sequence 96, Application US/09229007A
; Patent No. 6453242

; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preslected Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/09/229,007A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence
; OTHER INFORMATION: (F1, F2, F3) from SP1

US-09-229-007A-96

Query Match 58.1%; Score 36; DB 4; Length 21;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEMQRRADQLA 13
: |||: ||
Db 10 DELQRRSDHLS 20

RESULT 15

US-09-252-991A-24357
; Sequence 24357, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24357
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24357

Query Match 58.1%; Score 36; DB 4; Length 171;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LEMQRRADQ 11
|||: |||
Db 87 LEQFQRRLDQ 96

Search completed: March 4, 2004, 08:31:46
Job time : 22.8947 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 69.1053 Seconds
(without alignments)
53.153 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEMQRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query			Description
	Score	Match	Length DB ID	
1	62	100.0	13	AAB15583 Human SNA
2	62	100.0	64	AAG00764 Human sec
3	62	100.0	82	AAB15581 Human SNA
4	62	100.0	106	AAG03825 Human sec
5	62	100.0	106	AAG03826 Human sec
6	62	100.0	198	AAG00255 Synaptoso
7	62	100.0	199	AAG00263 Synaptoso
8	62	100.0	200	AAG00264 Synaptoso
9	62	100.0	201	AAG002637 Synaptoso
10	62	100.0	202	AAG00265 Synaptoso
11	62	100.0	203	AAG002636 Synaptoso
12	62	100.0	206	AAG03103 Synaptoso
13	62	100.0	206	AAG03426 Mouse syn
14	62	100.0	206	AAG03426 Mouse SNA
15	62	100.0	206	AAG00256 Synaptoso
16	62	100.0	206	AAG00261 Synaptoso
17	62	100.0	206	AAG00246 Synaptoso
18	62	100.0	206	AAG00253 SNARE hom
19	62	100.0	206	AAG002171 Synaptoso
20	62	100.0	206	AAG00266 Synaptoso
21	62	100.0	206	AAG002640 Synaptoso
22	62	100.0	206	AAG00258 Synaptoso
23	62	100.0	206	AAG00262 Synaptoso
24	62	100.0	206	AAG00259 Synaptoso
25	62	100.0	206	AAG00252 SNARE hom

26	62	100.0	206	AAU00260 Synaptoso
27	62	100.0	206	AAU02638 Synaptoso
28	62	100.0	206	AAU02639 Synaptoso
29	62	100.0	206	AAU00257 Synaptoso
30	62	100.0	206	AAE36662 Human SNA
31	62	100.0	206	AAE36667 Rat VAMP-
32	62	100.0	206	AAE54280 Rat Prote
33	62	100.0	206	AAE54288 Rat Prote
34	62	100.0	206	AAE54276 Rat Prote
35	62	100.0	206	AAE54290 Human Pro
36	62	100.0	206	AAE54282 Rat Prote
37	62	100.0	206	AAE54274 Rat Prote
38	62	100.0	206	AAE54286 Human Pro
39	62	100.0	206	AAE54284 Rat Prote
40	62	100.0	206	AAE54272 Rat Prote
41	62	100.0	206	AAE54278 Rat Prote
42	44	71.0	252	ABP25533 Streptoco
43	44	71.0	252	ABU46723 Protein e
44	41	66.1	480	AAB96534 Putative
45	40	64.5	312	ABB78803 Intermedi

ALIGNMENTS

RESULT 1
ID AAB15583 standard; peptide; 13 AA.
XX
AC AAB15583;
XX
DT 02-MAR-2001 (first entry)
XX
DB Human SNAP-25 N-terminal peptide #3.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN WO200064932-A1.
XX
PD 02-NOV-2000.
XX
PF 18-FEB-2000; 2000WO-ES000058.
XX
PR 23-APR-1999; 99ES-00000844.
XX
XX (LIPO-) LIPOTEC SA.
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;
XX
DR WPI; 2001-007091/01.
XX
XX New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders.
XX
PS Claim 9; Page 32; 40pp; Spanish.
XX
CC The invention relates to new peptides comprising 3-30 contiguous amino
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AAB15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
XX neurodegenerative disorders
SQ Sequence 13 AA;

Query Match 100.0%; Score 62; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
 |||||
 Db 1 ELEMQRADQLA 13

RESULT 2
 AAG00764
 ID AAG00764 standard; protein; 64 AA.
 XX AC AAG00764;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 4845.
 XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 XX KW gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.
 XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX DR WPI; 2000-500381/45.
 XX DR N-PSDB; AAC00770.
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX PS Claim 13; SEQ ID NO 4845; 71pp + Sequence Listing; English.
 XX CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX SQ Sequence 64 AA;

Query Match 100.0%; Score 62; DB 3; Length 64;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
 |||||
 Db 10 ELEMQRADQLA 22

RESULT 3
 AAB15581

ID AAB15581 standard; peptide; 82 AA.
 XX AC AAB15581;
 XX DT 02-MAR-2001 (first entry)
 XX DE Human SNAP-25 N-terminal peptide #1.
 XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
 KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
 KW neurodegenerative disorder.
 XX OS Homo sapiens.
 XX PN WO200064932-A1.
 XX PD 02-NOV-2000.
 XX PF 18-FEB-2000; 2000WO-ES000058.
 XX PR 23-APR-1999; 99ES-00000844.
 XX PA (LIPO-) LIPOTEC SA.
 XX PI Blandes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
 PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
 PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
 PI Perez Pava E;
 XX DR WPI; 2001-007091/01.
 XX PT New peptides containing amino acid sequences from known proteins for
 PT treatment of neurological disorders.
 XX PS Claim 1; Page 31; 40pp; Spanish.
 XX CC The invention relates to new peptides comprising 3-30 contiguous amino
 CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
 CC protein 25). The peptides AAB15581-B15586 represent examples of the
 CC peptides of the invention. The peptides have neuronal exocytosis
 CC inhibitory activity and are used for treatment of facial wrinkles and
 CC asymmetry and pathological neuronal exocytosis-mediated pathological
 CC disorders and alterations manifested e.g. by spasms and neurological and
 CC neurodegenerative disorders
 XX SQ Sequence 82 AA;

Query Match 100.0%; Score 62; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
 |||||
 Db 9 ELEMQRADQLA 21

RESULT 4
 AAG03825
 ID AAG03825 standard; protein; 106 AA.
 XX AC AAG03825;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 7906.
 XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX

PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
DR N-PSDB; AAC03831.
XX
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 7906; 71pp + Sequence Listing; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 62; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
Db |||||
10 ELEMORRADQLA 22

RESULT 5
AAG03826
ID AAG03826 standard; protein; 106 AA.
XX
AC AAG03826;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 7907.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
XX Homo sapiens.
OS
XX EP1033401-A2.
PN
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX WPI; 2000-500381/45.
DR N-PSDB; AAC03832.
XX

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 7907; 71pp + Sequence Listing; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 62; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQLA 13
Db |||||
10 ELEMORRADQLA 22

RESULT 6
AAU00255
ID AAU00255 standard; protein; 198 AA.
XX
AC AAU00255;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.
XX
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200118038-A2.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-GB003196.
XX
XX 20-AUG-1999; 99US-0149993P.
PR
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
PI
XX WPI; 2001-226739/23.
DR
XX
PT Treating a patient suffering from poisoning or at risk of poisoning by a
PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.
XX
XX Example 1; Page; 131pp; English.
PS
XX The sequence represents the amino acid sequence of synaptosomal-
CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new

CC method of treating a patient suffering from poisoning or at risk of
CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
CC to a cell of the patient, where the SNARE is resistant to proteolysis by
CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
CC treating a patient in need of inhibition of SNARE-dependent exocytosis
CC from a cell capable of performing SNARE-dependent exocytosis, comprises
CC supplying a fragment, variant, fusion or derivative of a SNARE or an
CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
CC useful in the manufacture of a medicament for the treatment of a patient
CC suffering from poisoning or at risk of poisoning by clostridial toxin,
CC e.g. from botulism or tetanus. The fragment, variant, fusion or
CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
CC polynucleotide encoding either of these SNARE polypeptides are useful in
CC the manufacture of medicament for the treatment of a patient in need of
CC inhibition of SNARE-dependent exocytosis from a cell capable of
CC performing SNARE-dependent exocytosis. The method of treatment is
CC relatively fast, thus alleviating the symptoms when most severe and
CC taking the patient out of critical state. Note: The present sequence is
CC not shown in the specification but is derived from the mouse SNAP-25
CC sequence given in figure 8 (see AAU00246)

XX
SQ Sequence 198 AA;

Query Match 100.0%; Score 62; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
Db |||||
10 ELEMQRADQLA 22

RESULT 7
AAU00263
ID AAU00263 standard; protein; 199 AA.
XX
AC AAU00263;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synaptosomal-associated protein, SNAP25, mutant 1-199(R198T).
XX
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
FT
XX WO200118038-A2.
PN
XX 15-MAR-2001.
PD
XX 18-AUG-2000; 2000WO-GB003196.
PF
XX 20-AUG-1999; 99US-0149993P.
PR
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
PA
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
PI
XX WPI; 2001-226739/23.
DR
XX Treating a patient suffering from poisoning or at risk of poisoning by a

PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.

XX
XX Example 1; Page; 131pp; English.

CC The sequence represents the amino acid sequence of synaptosomal-
CC associated protein, SNAP25, mutant 1-199(R198T), used in a new method of
CC treating a patient suffering from poisoning or at risk of poisoning by a
CC clostridial toxin, comprising supplying a SNARE (soluble (N-
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
CC a cell of the patient, where the SNARE is resistant to proteolysis by the
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
CC capable of performing SNARE-dependent exocytosis, comprises supplying a
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
CC or a recombinant polynucleotide encoding the SNARE is useful in the
CC manufacture of a medicament for the treatment of a patient suffering from
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
CC botulism or tetanus. The fragment, variant, fusion or derivative of a
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
CC either of these SNARE polypeptides are useful in the manufacture of
CC medicament for the treatment of a patient in need of inhibition of SNARE-
CC dependent exocytosis from a cell capable of performing SNARE-dependent
CC exocytosis. The method of treatment is relatively fast, thus alleviating
CC the symptoms when most severe and taking the patient out of critical
CC state. Note: The present sequence is not shown in the specification but
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
CC AAU00246)

XX
SQ Sequence 199 AA;

Query Match 100.0%; Score 62; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMQRADQLA 13
Db |||||
10 ELEMQRADQLA 22

RESULT 8
AAU00264
ID AAU00264 standard; protein; 200 AA.
XX
AC AAU00264;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synaptosomal-associated protein, SNAP25, mutant 1-200(R198T).
XX
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
FT
XX WO200118038-A2.
PN
XX 15-MAR-2001.
PD
XX 18-AUG-2000; 2000WO-GB003196.
PF
XX 20-AUG-1999; 99US-0149993P.
PR
XX

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI WPI; 2001-226739/23.
 XX
 DR Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 PT
 XX Example 1; Page; 131pp; English.
 PS
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-200(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 200 AA;
 Query Match 100.0%; Score 62; DB 4; Length 200;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEEMQRRADQLA 13
 DB |||||
 10 ELEEMQRRADQLA 22
 RESULT 9
 AAU02637
 ID AAU02637 standard; protein; 201 AA.
 XX
 AC AAU02637;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 XX
 PN WO200118038-A2.

XX 15-MAR-2001.
 PD
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI WPI; 2001-226739/23.
 DR
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 PT
 XX Example 1; Page; 131pp; English.
 PS
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 201 AA;
 Query Match 100.0%; Score 62; DB 4; Length 201;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEEMQRRADQLA 13
 DB |||||
 10 ELEEMQRRADQLA 22
 RESULT 10
 AAU00265
 ID AAU00265 standard; protein; 202 AA.
 XX
 AC AAU00265;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-202(R198T).
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.

OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 XX
 PN WO200118038-A2.
 XX
 PD 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI
 XX WPI; 2001-226739/23.
 DR
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-202(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 202 AA;
 Query Match 100.0%; Score 62; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 Db |||||
 10 ELEMORRADQLA 22
 RESULT 11
 AAU02636
 ID AAU02636 standard; protein; 203 AA.
 XX
 AC AAU02636;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-203 (R198T).
 XX

KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mitein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 XX
 PN WO200118038-A2.
 XX
 PD 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI
 XX WPI; 2001-226739/23.
 DR
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 203 AA;
 Query Match 100.0%; Score 62; DB 4; Length 203;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 Db |||||
 10 ELEMORRADQLA 22
 RESULT 12
 AAU0103
 ID AAU0103 standard; peptide; 206 AA.

XX AAW30103;
 AC
 XX
 DT 06-APR-1998 (first entry)
 XX
 DE Synaptosomal associated protein.
 XX
 DE Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX
 OS Homo sapiens.
 XX
 PN WO9734620-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US004393.
 XX
 PR 18-MAR-1996; 96US-0013599P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Montal M;
 XX
 DR WPI; 1997-479986/44.
 XX
 XX Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neuro:transmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 XX
 PS Disclosure; Page 27-28; 61pp; English.
 XX
 CC This sequence represents the human 25 kD synaptosomal associated protein
 CC (SNAP-25), which is an inhibitory agent of the invention. The agents of
 CC the invention inhibit secretion of neurotransmitter from neuronal cells
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20
 CC amino acids (aa) all of which correspond substantially to any one of
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
 CC catecholamine secretion from bovine chromaffin cells at a concentration
 CC of 10 microm, especially 0.25 microm, or less. (I) are used, as a
 CC replacement for Clostridium toxin, to inhibit release of
 CC neurotransmitters from synaptic vesicles, specifically for reducing
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
 CC intracellular distribution of (I). Compounds for delivering the drug to
 CC neural cells provide targeted drug delivery, e.g. of substance P to brain
 CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
 CC toxic or immunogenic and are more readily available. Their therapeutic
 CC effect lasts for several days or weeks, so lower doses or less frequent
 CC treatments are required
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 62; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 |||||
 Db 10 ELEMORRADQLA 22
 |||||
 RESULT 13
 AAW43426
 ID AAW43426 standard; protein; 206 AA.
 XX
 AC AAW43426;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Mouse synaptosomal-associated protein-25.
 XX

KW Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;
 KW neurotransmitter; presynaptic membrane; central nervous system; tumour;
 KW neurodegenerative disease; hormonal disorder; immunological disorder.
 XX
 OS Mus sp.
 XX
 PN US5693476-A.
 XX
 PD 02-DEC-1997.
 XX
 PF 24-FEB-1995; 95US-00393985.
 XX
 PR 24-FEB-1995; 95US-00393985.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Scheller RH;
 XX
 DR WPI; 1998-031743/03.
 DR N-PSDB; AAV01554.
 XX
 XX Screening assay for modulators of syntaxin binding - using peptide
 PT comprising binding site of syntaxin, for identifying drugs useful for
 PT treating CNS disorders, neuro-degenerative diseases, etc.
 XX
 PS Disclosure; Col 67-72; 57pp; English.
 XX
 CC This amino acid sequence represents the mouse synaptosomal-associated
 CC protein of 25 kD (SNAP-25). The invention relates to a method for
 CC identifying a compound capable of affecting the binding of a syntaxin-
 CC binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to
 CC syntaxin. The method comprises measuring the effect of the test compound
 CC on the extent of binding between the SBP and the SBP-binding site on
 CC syntaxin. The method can be used for identifying drugs capable of
 CC inhibiting or stimulating neurotransmitter release at the active zones of
 CC presynaptic membranes, which may be useful for treating CNS disorders,
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or
 CC immunological disorders or tumours
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 62; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 |||||
 Db 10 ELEMORRADQLA 22
 |||||
 RESULT 14
 AAW79198
 ID AAW79198 standard; protein; 206 AA.
 XX
 AC AAW79198;
 XX
 DT 25-NOV-1998 (first entry)
 XX
 DE Mouse SNAP-25 polypeptide.
 XX
 KW Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking;
 KW calcium-regulated secretion; secretory vesicle; secretory process; brain;
 KW neurotransmitter release; presynaptic membrane; CNS disorder; depression;
 KW Parkinson's disease; endocrine system; hormonal imbalance; cell division;
 KW thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;
 KW immune system; antigen processing; immunomodulator; viral processing;
 KW central nervous system; vesicular release; affective disorder; human;
 KW anti-tumour application; membrane trafficking regulation; mouse.
 XX
 OS Mus sp.
 XX
 PN WO9838210-A2.
 XX

PD 03-SEP-1998.
 XX
 PF 26-FEB-1998; 98WO-US003789.
 XX
 PR 26-FEB-1997; 97US-0039159P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Bean AJ, Scheller RH;
 XX
 DR WPI; 1998-481140/41.
 DR N-PSDB; AAV57558.
 XX
 PT New isolated Hrs-2 nucleotidase - used in assays to identify compounds
 PT capable of modulating calcium-regulatory secretion of secretory vesicles,
 PT such as in neurotransmitter release.
 XX
 PS Claim 16; Page 42-44; 55pp; English.
 XX
 CC This represents a mouse SNAP-25 polypeptide, a component of the protein
 CC polypeptides thought to underlie vesicle docking and fusion. The
 CC invention provides rat and human Hrs-2 polypeptides which are ATP-
 CC preferring nucleotidase that associate with SNAP-25. For identifying a
 CC compound capable of modulating calcium-regulated secretion of secretory
 CC vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2
 CC polypeptide, in the presence and absence of a test compound. The effect
 CC of the test compound on the extent of binding between the SNAP-25 and Hrs
 CC -2 polypeptides are measured and a compound is identified as effective if
 CC its measured effect on the extent of binding is above a threshold level.
 CC The products can be used for identifying drugs capable of affecting
 CC secretory processes, such as neurotransmitter release at the active zones
 CC of presynaptic membranes. Such drugs can be used for treating disorders
 CC or conditions of the central nervous system by selectively enhancing or
 CC inhibiting vesicular release in specific areas of the brain, including
 CC affective disorders (e.g. depression), disorders of thought (e.g.
 CC schizophrenia) and degenerative disorders (Parkinson's disease), as well
 CC as applications such as anaesthesia. The drugs can also be used
 CC therapeutically in other systems such as the endocrine system for
 CC treatment of hormonal imbalances, the immune system for intervention in
 CC antigen processing, secreted immunomodulators, and viral processing, as
 CC well as anti-tumour applications, such as regulation of membrane
 CC trafficking during rapid cell division
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 62; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELEEMQRRADQLA 13
 |||||
 Db 10 ELEEMQRRADQLA 22
 RESULT 15
 AAU00256
 ID AAU00256 standard; protein; 206 AA.
 XX
 AC AAU00256;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant Q197A/R198A.
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Ala"
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Ala"
 FT
 XX WO200118038-A2.
 PN
 XX 15-MAR-2001.
 PD
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI
 XX WPI; 2001-226739/23.
 DR
 XX
 PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant Q197A/R198A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 62; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELEEMQRRADQLA 13
 |||||
 Db 10 ELEEMQRRADQLA 22

Search completed: March 4, 2004, 08:27:50
 Job time : 70.1053 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 6.63158 Seconds
(without alignments)
47.111 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	206	1 SN25 HUMAN	P13795 homo sapien
2	27	90.0	180	1 STN3 CHICK	O93388 gallus gall
3	27	90.0	219	1 IF6 METMA	O8pyq3 methanosarc
4	27	90.0	303	1 PQOB PSEFL	P55172 pseudomonas
5	27	90.0	303	1 PQOB PSEPK	O88qv5 pseudomonas
6	27	90.0	303	1 PQOB PSESM	O88a81 pseudomonas
7	27	90.0	328	1 COAA COREF	O8fqr2 corynebacte
8	27	90.0	388	1 LHX9 HUMAN	O9nq69 homo sapien
9	27	90.0	388	1 LHX9 MOUSE	O9wuh2 mus musculu
10	27	90.0	390	1 TFT1 MOUSE	O08970 mus musculu
11	27	90.0	450	1 PUR8 PYRAB	O9uz99 pyrococcus
12	27	90.0	450	1 PUR8 PYRHO	O58582 pyrococcus
13	27	90.0	509	1 GATE TREPA	O83984 treponema p
14	27	90.0	568	1 ESR2 ONCMY	P57782 oncorhynchu
15	27	90.0	613	1 ILVD CORGL	O8nqz9 corynebacte
16	27	90.0	622	1 YAE7 YEAST	P39723 saccharomyc
17	27	90.0	636	1 PAPB HUMAN	O9nrj5 homo sapien
18	27	90.0	641	1 PAPB MOUSE	O9wvp6 mus musculu
19	27	90.0	660	1 PAP HUMAN	P51003 homo sapien
20	27	90.0	677	1 GCP3 MOUSE	P58854 mus musculu
21	27	90.0	727	1 YM29 YEAST	O03792 saccharomyc
22	27	90.0	738	1 PAP BOVIN	P25500 bos taurus
23	27	90.0	738	1 PAP MOUSE	O61183 mus musculu
24	27	90.0	809	1 HELI EBV	P03214 epstein-bar
25	27	90.0	907	1 GCP3 HUMAN	O96cws homo sapien
26	27	90.0	960	1 FGDI MOUSE	P52734 mus musculu
27	27	90.0	961	1 FGDI HUMAN	P98174 homo sapien
28	27	90.0	1052	1 BUIB MOUSE	O9zls0 mus musculu
29	27	90.0	2133	1 FAB FIG	P12263 sus scrofa
30	26	86.7	200	1 RHO2 SCHPO	Q10133 schizosacch
31	26	86.7	204	1 SNXN HUMAN	O96l93 homo sapien
32	26	86.7	261	1 NEF SIVSP	P19501 simian immu
33	26	86.7	340	1 ADHA RHIME	O31186 rhizobium m

RESULT 1

SN25_HUMAN	34	26	86.7	424	1	CG1E HEMPU	O15995 hemicentrot
ID SN25_HUMAN	35	26	86.7	453	1	YUQP CAEEL	Q19895 caenorhabdi
AC P13795; P36974; P70557; P70558; Q8IXK3; Q96FM2; Q9BR45;	36	26	86.7	482	1	CATA BORPE	P48062 bordetella
DT 01-JAN-1990 (Rel. 13, Created)	37	26	86.7	493	1	SYE PSEPK	Q881f6 pseudomonas
DT 01-FEB-1991 (Rel. 17, Last sequence update)	38	26	86.7	493	1	SYE PSESM	Q884c8 pseudomonas
DT 15-MAR-2004 (Rel. 43, Last annotation update)	39	26	86.7	507	1	PSBB SYN3	P05429 synechocyst
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).	40	26	86.7	533	1	IMA5_MOUSE	O35345 mus musculu
GN SNAP25 OR SNAP.	41	26	86.7	535	1	HR65_CHITE	O9uin0 chironomus
OS Homo sapiens (Human),	42	26	86.7	579	1	NCOS_HUMAN	O9hcd5 homo sapien
OS Macaca mulatta (Rhesus macaque),	43	26	86.7	579	1	NCOS_MOUSE	O91w39 mus musculu
OS Mus musculus (Mouse),	44	26	86.7	608	1	TERM_ADECC	Q65947 canine aden
OS Rattus norvegicus (Rat), and	45	26	86.7	628	1	GATE_PYRFU	Q8u0w9 pyrococcus
OS Gallus gallus (Chicken).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
OX NCBI_TaxID=9606, 9544, 10090, 10116, 9031;							
[1]							
RN							
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).							
RC SPECIES=Human; TISSUE=Brain;							
RX MEDLINE=94156217; PubMed=8112622;							
RA Bark I.C., Wilson M.C.;							
RT "Human cDNA clones encoding two different isoforms of the nerve							
terminal protein SNAP-25.";							
RL Gene 139:291-292 (1994).							
[2]							
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).							
RC SPECIES=Human; TISSUE=Brain;							
RX MEDLINE=94333829; PubMed=8056350;							
RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;							
RT "Cloning and sequence analysis of the human SNAP25 cDNA.";							
RL Gene 145:313-314 (1994).							
[3]							
RN							
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.							
RC SPECIES=Human; TISSUE=Skeletal muscle;							
RX MEDLINE=96332494; PubMed=8760387;							
RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,							
Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,							
Frenkel M.J., Ward C.W.;							
RT "Insulin-responsive tissues contain the core complex protein SNAP-25							
(synaptosomal-associated protein 25) A and B isoforms in addition to							
syntaxin 4 and synaptobrevins 1 and 2.";							
RL Biochem. J. 317:945-954 (1996).							
[4]							
RN							
RP SEQUENCE FROM N.A.							
RC SPECIES=Human;							
RX MEDLINE=21638749; PubMed=11780052;							
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,							
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,							
Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,							
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,							
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,							
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,							
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,							
Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,							
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,							

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leheslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McElay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Human; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=BALB/c;
RX Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=BALB/c;
RX Oryler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
RA Bloom F.E., Wilson M.C.;
RT "The identification of a novel synaptosomal-associated protein,
RT SNAP-25, differentially expressed by neuronal subpopulations.";
RL J. Cell Biol. 109:3039-3052(1999).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=ILS, and ISS;
RX MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-throughput sequence identification of gene coding variants
RT with alcohol-related QTLs.";
RL Mamm. Genome 12:657-663(2001).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierzki R.M., King B.L.,
RA Nagatoya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birhey E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
RA Strausberg R.L.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RC SPECIES=Rat;
RA Kataoka M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Rat; TISSUE=Brain;
RA Cho A.R., You K.H.;
RT "Cloning of the SNAP-25 gene from a rat brain cDNA library.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
RC SPECIES=Rat; TISSUE=Brain;
RX MEDLINE=99155074; PubMed=10037470;
RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
RT "SNARE complex proteins, including the cognate pair VAMP-2 and
RT syntaxin-4, are expressed in cultured oligodendrocytes.";
RL J. Neurochem. 72:988-998(1999).
RN [14]
RP SEQUENCE FROM N.A.
RC SPECIES=Chicken; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=1992470;
RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.;
RT "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
RN [15]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC SPECIES=Chicken;
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein.";
RL J. Mol. Biol. 233:67-76(1993).
RN [16]
RP PALMITOYLATION.
RC SPECIES=Rat;
RX MEDLINE=93100552; PubMed=1281490;
RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
RT methionine-rich polypeptide in rapid axonal transport and a major

Query Match 100.0%; Score 30; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 |||||
 DB 12 EEMQRR 17

RESULT 2

STN3 CHICK STANDARD; PRT; 180 AA.
 AC O93388;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Stathmin 3 (SCG10-like protein) (Neuroplasticin-2).
 GN STMN3 OR SCLIP OR NPC2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]

SEQUENCE FROM N.A.

RA Lutjens R., Osen-Sand A., Grenningloh G.;
 RT "Characterization of a new member of the SCG10/stathmin family of
 genes.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the stathmin family.
 CC

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EMBL; AF076982; AAC27325.1; -.

InterPro; IPR000956; Stathmin.

Pfam; PF00836; Stathmin; 1.

PRINTS; PR00345; STATHMIN.

PROSITE; PS00563; STATHMIN_1; 1.

PROSITE; PS01041; STATHMIN_2; 1.

Coiled coil.

FT DOMAIN 75 179 COILED COIL (POTENTIAL).

SEQUENCE 180 AA; 20994 MW; DE3554E4EBDEF5E CRC64;

Query Match 90.0%; Score 27; DB 1; Length 180;
 Best Local Similarity 83.3%; Pred. No. 58;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 |||||
 DB 83 EELQRR 88

RESULT 3

IF6 METMA STANDARD; PRT; 219 AA.
 AC Q8PYQ3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Translation initiation factor 6 (aIF-6).
 GN EIF6 OR MM0807.

OS Methanosarcina mazel (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2209;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=22120827; PubMed=12125824;
 RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wierzer A., Baumer S., Jacobi C.,
 RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
 RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
 RA Fritz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazel: evidence for lateral gene
 RT transfer between Bacteria and Archaea.";
 RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
 CC -!- FUNCTION: Binds to the 60S ribosomal subunit and prevents its
 CC association with the 40S ribosomal subunit to form the 80S
 CC initiation complex (By similarity).
 CC -!- SIMILARITY: Belongs to the eIF-6 family.
 CC

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 CC

EMBL; AE013306; AAM30503.1; -.

HAMAP; MF 00032; -; 1.

InterPro; IPR002769; eIF6.

Pfam; PF01912; eIF6; 1.

ProDom; PD006880; eIF6; 1.

KW Initiation factor; Protein biosynthesis; Complete proteome.

SEQUENCE 219 AA; 23114 MW; 06E0E1FC24FDEF25 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 219;
 Best Local Similarity 83.3%; Pred. No. 71;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 |||||
 DB 77 EEMQRR 82

RESULT 4

PQB PSEFL STANDARD; PRT; 303 AA.
 AC P55172;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein B (Pyrroloquinoline quinone
 DE biosynthesis protein B).
 GN PQB.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]

SEQUENCE FROM N.A.

RP STRAIN=CHAO;

MEDLINE=96064397; PubMed=8526497;

Schnider U., Keel C., Defago G., Haas D.;

"Tns-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin.";
 RL Appl. Environ. Microbiol. 61:3856-3864 (1995).

CC -!- FUNCTION: May be involved in the transport of PQQ or its precursor
 CC to the periplasm (By similarity).

CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.

CC -!- SIMILARITY: Belongs to the pqqB family.

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DR EMBL; X87299; CAA60733.1; -.
 DR PIR; S58243; S58243.
 DR HAMAP; MF_00653; -; 1.
 KW PQQ biosynthesis; Transport.
 SQ SEQUENCE 303 AA; 33207 MW; 8D958BD1A9CD32F9 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 303;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 :|||||
 Db 227 DEMQRR 232

RESULT 5

PQQB_PSEPK STANDARD; PRT; 303 AA.
 AC Q88QV5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein B (Pyrroloquinoline quinone
 biosynthesis protein B).
 GN PQQB OR PP0379.
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moarrez A.,
 RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
 RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 CC -!- FUNCTION: May be involved in the transport of PQQ or its precursor
 CC to the periplasm (By similarity).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqB family.

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DR EMBL; X87299; CAA60733.1; -.
 DR TIGR; PP0379; -.
 DR HAMAP; MF_00653; -; 1.
 KW PQQ biosynthesis; Transport; Complete proteome.
 SQ SEQUENCE 303 AA; 33331 MW; 37A3653C6B52B01E CRC64;

Query Match 90.0%; Score 27; DB 1; Length 303;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 :|||||

Db 227 DEMQRR 232

RESULT 6

PQQB_PSESM STANDARD; PRT; 303 AA.
 AC Q88AB1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein B (Pyrroloquinoline quinone
 biosynthesis protein B).
 GN PQQB OR PSPT00512.
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RX MEDLINE=22834015; PubMed=12928499;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Daviden T., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Khouri H., Fedorova N., Tran B., Russell D., Berry K., Uterback T.,
 RA Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,
 RA Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,
 RA Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
 RA White O., Fraser C.M., Collmer A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 RT Pseudomonas syringae pv. tomato DC3000.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 CC -!- FUNCTION: May be involved in the transport of PQQ or its precursor
 CC to the periplasm (By similarity).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqB family.

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DR EMBL; AE016857; AAO54055.1; -.
 DR TIGR; PSPT00512; -.
 DR HAMAP; MF_00653; -; 1.
 KW PQQ biosynthesis; Transport; Complete proteome.
 SQ SEQUENCE 303 AA; 33326 MW; 2B6C41E02AF016CC CRC64;

Query Match 90.0%; Score 27; DB 1; Length 303;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 :|||||
 Db 227 DEMQRR 232

RESULT 7

COAA_COREF STANDARD; PRT; 328 AA.
 AC Q8FQR2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase).
 GN COAA OR CE1057.
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RL efficiens.";
RL Genome Res. 13:1572-1579 (2003).
CC -!- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -!- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the prokaryotic pantothenate kinase family.
CC -----
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CC -----
DR EMBL; AP005217; BAC17867.1; -.
DR HAMAP; MF_00215; -; 1.
DR InterPro; IPR004566; PanK bact.
DR InterPro; IPR006083; PRK_URK.
DR Pfam; PF00485; PRK; 1.
DR PIRSF; PIRSF000545; Pantothenate_kin; 1.
DR TIGRFAMs; TIGR00554; panK bact; 1.
KW Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
KW Complete proteome.
FT NP_BIND 113 120 ATP (POTENTIAL).
SQ SEQUENCE 328 AA; 37254 MW; E6737A57964DC2C5 CRC64;
Query Match 90.0%; Score 27; DB 1; Length 328;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
DB 152 EELQRR 157
RESULT 8
LHX9_HUMAN STANDARD; PRT; 388 AA.
ID LHX9_HUMAN Q9NQ69; Q9BYU6; Q9NQ70;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx9.
GN LHX9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21291005; PubMed=11397841;
RA Ottolenghi C., Moreira-Filho C., Mendonca B.B., Barbieri M.,
RA Fellous M., Berkovitz G.D., McElravey K.;
RT "Absence of mutations involving the LIM homeobox domain gene LHX9 in
RT 46,XY gonadal agenesis and dysgenesis.";
RL J. Clin. Endocrinol. Metab. 86:2465-2469 (2001).
CC -!- FUNCTION: Involved in gonadal development (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.

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CC -----
DR EMBL; AJ277915; CAB97493.1; -.
DR EMBL; AJ277916; CAB98128.1; ALT SEQ.
DR EMBL; AJ277917; CAB98128.1; JOINED.
DR EMBL; AJ277918; CAB98128.1; JOINED.
DR EMBL; AJ277919; CAB98128.1; JOINED.
DR EMBL; AJ277920; CAB98128.1; JOINED.
DR EMBL; AJ296272; CAC33174.1; -.
DR HSSP; P06601; 1FJL.
DR Genew; HGNC:14222; LHX9.
DR MIM; 606066; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00446; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc.
FT DOMAIN 62 114 LIM 1.
FT DOMAIN 124 177 LIM 2.
FT DNA_BIND 258 317 HOMEBOX.
SQ SEQUENCE 388 AA; 42903 MW; A4DC8B914D7C3B66 CRC64;
Query Match 90.0%; Score 27; DB 1; Length 388;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
DB 26 EEMERR 31
RESULT 9
LHX9_MOUSE STANDARD; PRT; 388 AA.
ID LHX9_MOUSE Q9WUH2; Q9YQ5; Q9YQ6; Q9QZ00; Q9WU44;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx9.
GN LHX9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-300 FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=99098964; PubMed=9880598;
RA Retaux S., Rogard M., Bach I., Failli V., Besson M.J.;
RT "Lhx9: a novel LIM-homeobox domain gene expressed in the developing
RT forebrain.";
RL J. Neurosci. 19:783-793 (1999).
RN [2]
RP SEQUENCE OF 11-388 FROM N.A.
RC STRAIN=NIH Swiss;
RX MEDLINE=99264291; PubMed=10330499;

RA Bertuzzi S., Porter F.D., Pitts A., Kumar M., Agulnick A., Wassif C.,
RA Westphal H.;
RT "Characterization of Lhx9, a novel LIM/homeobox gene expressed by the
RT pioneer neurons in the mouse cerebral cortex.";
RL Mech. Dev. 81:193-198(1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=20221375; PubMed=10756098;
RA Failli V., Rogard M., Mattei M.-G., Vernier P., Retaux S.;
RT "Lhx9 and Lhx9alpha LIM-homeodomain factors: genomic structure,
RT expression patterns, chromosomal localization, and phylogenetic
RT analysis.";
RL Genomics 64:307-317(2000).
CC -!- FUNCTION: Involved in gonadal development.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=Q9WUH2-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q9WUH2-2; Sequence=VSP_003111;
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
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CC -----
DR EMBL; AF134761; AAD30110.1; -;
DR EMBL; AF113518; AAD22008.1; -;
DR EMBL; AJ243851; CAB59907.1; -;
DR EMBL; AJ243852; CAB59908.1; -;
DR EMBL; AJ243853; CAB59908.1; JOINED.
DR EMBL; AJ243854; CAB59908.1; JOINED.
DR EMBL; AJ243855; CAB59908.1; JOINED.
DR EMBL; AJ243856; CAB59908.1; JOINED.
DR EMBL; AJ243857; CAB59909.1; -;
DR EMBL; AJ243853; CAB59909.1; JOINED.
DR EMBL; AJ243854; CAB59909.1; JOINED.
DR EMBL; AJ243855; CAB59909.1; JOINED.
DR EMBL; AJ243857; CAB59909.1; JOINED.
DR HSP; P06601; 1FJL.
DR TRANSFAC; T04192; -;
DR TRANSFAC; T04195; -;
DR MGD; MGI:1316721; Lhx9.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc; Alternative splicing.
FT DOMAIN 62 114
FT DOMAIN 124 177
FT DNA BIND 258 317
FT VARSPIC 304 388
FT VFWQNAKFRNLLRQENGVDKADGTSUPAPPSADSGAL
FT TTPGTATLTDLNPTVTVTVTISNMDSHEPGSPSTTLT
FT NLF -> GEQILGHYSQTSRLKIP (in isoform
FT Alpha).
FT /FTId=VSP_003111.

FT CONFLICT 49 49 A -> T (IN REF. 2).
FT CONFLICT 153 153 S -> F (IN REF. 2).
SQ SEQUENCE 388 AA; 42986 MW; C2D7326A68D87B32 CRC64;
Query Match 90.0%; Score 27; DB 1; Length 388;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
DB 26 EEMERR 31
RESULT 10
TFTI_MOUSE
ID TFTI_MOUSE STANDARD; PRT; 390 AA.
AC O08970;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tuftelin.
GN TUFTL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC STRAIN=Swiss Webster; TISSUE=Tooth;
RX MEDLINE=99053519; PubMed=9839784;
RA MacDougall M., Simmons D., Dodds A., Knight C., Luan X.,
RA Zeichner-David M., Zhang C., Ryu O.H., Qian Q., Simmer J.P., Hu C.-C.;
RT "Cloning, characterization, and tissue expression pattern of mouse
RT tuftelin cDNA.";
RL J. Dent. Res. 77:1970-1978(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=21590372; PubMed=11733143;
RA Mao Z., Shay B., Hekmati M., Fermon E., Taylor A., Dafni L.,
RA Heikinheimo K., Lustmann J., Fisher L.W., Young M.F., Deutsch D.;
RT "The human tuftelin gene: cloning and characterization.";
RL Gene 279:181-196(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 7-324 FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC STRAIN=Swiss Webster;
RX MEDLINE=97228909; PubMed=9074935;
RA Zeichner-David M., Vo H., Tan H., Diekwisch T., Berman B.,
RA Thienemann F., Alcocer M.D., Hsu P., Wang T., Eyna J., Caton J.,
RA Slavkin H.C., MacDougall M.;


```

RT "Timing of the expression of enamel gene products during mouse tooth
RT development.";
RL Int. J. Dev. Biol. 41:27-38(1997).
RN [5]
RP INTERACTION WITH TFIP11.
RC STRAIN=Swiss Webster; TISSUE=Tooth;
RX MEDLINE=20357353; PubMed=10806191;
RA Paine C.T., Paine M.L., Luo W., Okamoto C.T., Lyngstadaas S.P.,
RA Snead M.L.;
RT "A tuftelin-interacting protein (TIP39) localizes to the apical
RT secretory pole of mouse ameloblasts.";
RL J. Biol. Chem. 275:22284-22292(2000).
CC -!- FUNCTION: Involved in the mineralization and structural
CC organization of enamel.
CC -!- SUBUNIT: Interacts with TFIP11. May form oligomers.
CC -!- SUBCELLULAR LOCATION: Secreted at a very early stage of enamel
CC formation, concentrated at the dentin-enamel junction and tightly
CC bound to the surface of the growing crystallites (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=O08970-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O08970-2; Sequence=VSP_006687;
CC Name=3;
CC IsoId=O08970-3; Sequence=VSP_006687, VSP_006688;
CC -!- TISSUE SPECIFICITY: Ameloblasts, and also nonodontogenic tissues
CC including kidney, lung, liver and testis.
CC -!- DEVELOPMENTAL STAGE: Expressed in tooth from E13, the bud stage.
CC Continues to be expressed even when thick enamel is formed.
CC -!- SIMILARITY: Belongs to the tuftelin family.
CC
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CC
CC -----
DR EMBL; AF047704; AAC04577.1; -.
DR EMBL; BC019213; AAH19213.1; -.
DR EMBL; AF002860; AAB0891.1; -.
DR MGD; MGI:109572; Tuft1.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0030345; F:structural constituent of tooth enamel; ISS.
DR GO; GO:0030282; P:bone mineralization; ISS.
DR GO; GO:0042476; P:odontogenesis; ISS.
KW Biomaterialization; Coiled coil; Alternative splicing.
FT DOMAIN 88 126 COILED COIL (POTENTIAL).
FT DOMAIN 163 352 COILED COIL (POTENTIAL).
FT VARSPPLIC 21 45 Missing (in isoform 2 and isoform 3).
FT FTId=VSP_006687.
FT VARSPPLIC 96 356 Missing (in isoform 3).
FT FTId=VSP_006688.
SQ SEQUENCE 390 AA; 44576 MW; 968FA7BBE95DFEC1 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 390;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 230 EELQRR 235

RESULT 11
PUR8_PYRAB
ID PUR8_PYRAB STANDARD; PRT; 450 AA.
AC Q9UZ99;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

"Timing of the expression of enamel gene products during mouse tooth
development.";
Int. J. Dev. Biol. 41:27-38(1997).
[5]
INTERACTION WITH TFIP11.
STRAIN=Swiss Webster; TISSUE=Tooth;
MEDLINE=20357353; PubMed=10806191;
Paine C.T., Paine M.L., Luo W., Okamoto C.T., Lyngstadaas S.P.,
Snead M.L.;
"A tuftelin-interacting protein (TIP39) localizes to the apical
secretory pole of mouse ameloblasts.";
J. Biol. Chem. 275:22284-22292(2000).
-!- FUNCTION: Involved in the mineralization and structural
organization of enamel.
-!- SUBUNIT: Interacts with TFIP11. May form oligomers.
-!- SUBCELLULAR LOCATION: Secreted at a very early stage of enamel
formation, concentrated at the dentin-enamel junction and tightly
bound to the surface of the growing crystallites (By similarity).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1;
IsoId=O08970-1; Sequence=Displayed;
Name=2;
IsoId=O08970-2; Sequence=VSP_006687;
Name=3;
IsoId=O08970-3; Sequence=VSP_006687, VSP_006688;
-!- TISSUE SPECIFICITY: Ameloblasts, and also nonodontogenic tissues
including kidney, lung, liver and testis.
-!- DEVELOPMENTAL STAGE: Expressed in tooth from E13, the bud stage.
Continues to be expressed even when thick enamel is formed.
-!- SIMILARITY: Belongs to the tuftelin family.

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EMBL; AF047704; AAC04577.1; -.
EMBL; BC019213; AAH19213.1; -.
EMBL; AF002860; AAB0891.1; -.
MGD; MGI:109572; Tuft1.
GO; GO:0005576; C:extracellular; ISS.
GO; GO:0030345; F:structural constituent of tooth enamel; ISS.
GO; GO:0030282; P:bone mineralization; ISS.
GO; GO:0042476; P:odontogenesis; ISS.
Biomaterialization; Coiled coil; Alternative splicing.
DOMAIN 88 126 COILED COIL (POTENTIAL).
DOMAIN 163 352 COILED COIL (POTENTIAL).
VARSPPLIC 21 45 Missing (in isoform 2 and isoform 3).
FTId=VSP_006687.
VARSPPLIC 96 356 Missing (in isoform 3).
FTId=VSP_006688.
SEQUENCE 390 AA; 44576 MW; 968FA7BBE95DFEC1 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 390;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 230 EELQRR 235

RESULT 12
PUR8_PYRHO
ID PUR8_PYRHO STANDARD; PRT; 450 AA.
AC O58582;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL).
GN PURB OR PYRAB12550 OR PAB0829.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
CC -!- CATALYTIC ACTIVITY: N(6)-(1,2-dicarboxyethyl)AMP = fumarate + AMP.
CC -!- CATALYTIC ACTIVITY: (S)-2-[5-amino-1-(5-phospho-D-
CC ribosyl)imidazole-4-carboxamido]succinate = fumarate + 5-amino-1-
CC (5-phospho-D-ribose)imidazole-4-carboxamide.
CC -!- PATHWAY: De novo purine biosynthesis; eighth step.
CC -!- SIMILARITY: Belongs to the lyase 1 family. Adenylosuccinate lyase
CC subfamily.
CC
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CC
CC -----
EMBL; AJ248287; CAB50160.1; -.
PIR; C75033; C75033.
HSSP; Q9X010; 1C3C.
DR InterPro; IPR000362; Fumarate_lyase.
DR InterPro; IPR008948; L-Aspartase-like.
DR InterPro; IPR004769; Pur_lyase.
DR Pfam; PF00206; lyase 1; 1.
DR PRINTS; PR00149; FUMRATELYASE.
DR TIGRFSMs; TIGR00928; purB; 1.
DR PROSITE; PS00163; FUMARATE_LYASES; 1.
KW Purine biosynthesis; Lyase; Complete proteome.
FT ACT_SITE 76 76 ACID (BY SIMILARITY).
FT ACT_SITE 149 149 BASE (BY SIMILARITY).
SQ SEQUENCE 450 AA; 51455 MW; 82A3C0131455CDBD CRC64;

Query Match 90.0%; Score 27; DB 1; Length 450;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 443 EEMERR 448

RESULT 12
PUR8_PYRHO
ID PUR8_PYRHO STANDARD; PRT; 450 AA.
AC O58582;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL).
GN PURB OR PH0852.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;

```

RA Kwarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo H. Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -!- CATALYTIC ACTIVITY: N(6)-(1,2-dicarboxylethyl)AMP = fumarate + AMP.
 CC -!- CATALYTIC ACTIVITY: (S)-2-[5-amino-1-(5-phospho-D-
 ribosyl)imidazole-4-carboxamido]succinate = fumarate + 5-amino-1-
 (5-phospho-D-ribose)imidazole-4-carboxamide.
 CC -!- PATHWAY: De novo purine biosynthesis; eighth step.
 CC -!- SIMILARITY: Belongs to the lyase 1 family. Adenylosuccinate lyase
 subfamily.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AP000003; BAA29946.1; -.
 DR PIR; H71135; H71135.
 DR HSSP; Q9X010; 1C3C.
 DR InterPro; IPR000362; Fumarate_lyase.
 DR InterPro; IPR008948; L-Aspartase-like.
 DR InterPro; IPR004769; Pur_lyase.
 DR Pfam; PF00206; lyase 1; 1.
 DR PRINTS; PR00149; FUMRATLYASE.
 DR TIGRFAMS; TIGR00928; purB; 1.
 DR PROSITE; PS00163; FUMARATE_LYASES; 1.
 DR Purine biosynthesis; Lyase; Complete proteome.
 KW ACT_SITE 76 76 ACID (BY SIMILARITY).
 FT ACT_SITE 149 149 BASE (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 51644 MW; A700A652ADB822BC CRC64;

Query Match 90.0%; Score 27; DB 1; Length 450;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 |||||
 Db 443 EEMERR 448

RESULT 13
 GATE_TREPA STANDARD; PRT; 509 AA.
 AC 083984;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
 (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
 GN GATB OR TP1021.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Gariand S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;

RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete.";
 RL Science 281:375-388(1998).
 CC -!- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
 or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
 tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
 of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
 takes place in the presence of glutamine and ATP through an
 activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
 similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
 + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
 CC -!- CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA(Asn) + L-glutamine = ADP
 + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate.
 CC -!- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
 CC -!- SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE001269; AAC65971.1; -.
 DR PIR; A71254; A71254.
 DR TIGR; TP1021; -.
 DR HAMAP; MF_00121; -; 1.
 DR InterPro; IPR004413; GatB.
 DR InterPro; IPR006107; GatB_cent.
 DR InterPro; IPR006075; GatB_N.
 DR InterPro; IPR003789; GatB_Yqey.
 DR Pfam; PF01162; GatB; 1.
 DR Pfam; PF02934; GatB_N; 1.
 DR Pfam; PF02637; GatB_Yqey; 1.
 DR TIGRFAMS; TIGR00133; GatB; 1.
 DR PROSITE; PS01234; GATB; 1.
 KW Protein biosynthesis; Ligase; Complete proteome.
 SQ SEQUENCE 509 AA; 56865 MW; C28B9012236BF52 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 509;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
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 Db 272 EEMQRR 277

RESULT 14
 ESR2_ONCMY STANDARD; PRT; 568 AA.
 ID ESR2_ONCMY STANDARD; PRT; 568 AA.
 AC P57782;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estrogen receptor beta (ER-beta).
 GN ESR2 OR NR3A2.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haug M., Ackermann G., Fent K.;
 RT "Molecular cloning of an estrogen receptor beta subtype from rainbow
 trout.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
 ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.

CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-
CC ALPHA (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
CC subfamily.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ289883; CAC06714.1; -.
CC HSSP; P03372; 1ERR.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 177 MODULATING.
FT DNA_BIND 178 243 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 178 198 C4-TYPE.
FT ZN_FING 214 238 C4-TYPE.
FT DOMAIN 244 568 STEROID-BINDING.
SQ SEQUENCE 568 AA; 63813 MW; F7A7BD7B3B2C2804 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 568;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
||:||||
Db 456 EELQRR 461

RESULT 15
ID ILVD CORGL STANDARD; PRT; 613 AA.
AC Q8NQZ9; Q9RM73;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
GN ILVD OR CGL1268.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Ondrejškova A., Eggeling L., Sahm H.;
RT "Cloning and molecular analysis of the ilvD gene of Corynebacterium
RT glutamicum."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-oxobutanoate + H(2)O.
CC -!- COFACTOR: Binds 1 4Fe-4S cluster (Potential).
CC -!- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
CC -!- SIMILARITY: Belongs to the ilvD / edd family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ012293; CAB57218.1; -.
CC EMBL; AP005278; BAB98661.1; -.
DR HAMAP; MF_00012; -; 1.
DR InterPro; IPR004404; ILVD.
DR InterPro; IPR000581; ILVD_EDD_family.
DR Pfam; PF00920; ILVD_EDD; 1.
DR ProDom; PD002691; ILVD_EDD_family; 2.
DR TIGRfam; TIGR00110; ilvD; 1.
DR PROSITE; PS00886; ILVD_EDD_1; 1.
DR PROSITE; PS00887; ILVD_EDD_2; 1.
KW Branched-chain amino acid biosynthesis; Lyase; Iron; Iron-sulfur;
KW 4Fe-4S; Complete proteome.
FT METAL 122 122 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 197 197 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT CONFLICT 78 78 MISSING (IN REF. 1).
FT CONFLICT 157 158 DG -> ER (IN REF. 1).
FT CONFLICT 188 188 A -> R (IN REF. 1).
FT CONFLICT 332 332 G -> R (IN REF. 1).
SQ SEQUENCE 613 AA; 64674 MW; B422D5256ACDB250 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 613;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
||:||||
Db 565 EELQRR 570

Search completed: March 4, 2004, 08:25:55
Job time : 7.63158 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:20 ; Search time 17.3684 Seconds
(without alignments)
72.944 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	206	10	US-09-942-024-2
2	30	100.0	206	10	US-09-942-024-7
3	30	100.0	206	10	US-09-942-024-12
4	30	100.0	206	10	US-09-942-098-2
5	30	100.0	206	10	US-09-942-098-7
6	30	100.0	206	10	US-09-942-098-12
7	30	100.0	249	10	US-09-942-024-16
8	30	100.0	249	10	US-09-942-098-16
9	27	90.0	35	13	US-10-029-217A-21
10	27	90.0	82	14	US-10-082-828A-255
11	27	90.0	214	9	US-09-925-300-1287
12	27	90.0	240	14	US-10-029-386-33812
13	27	90.0	245	9	US-09-925-299-791
14	27	90.0	245	10	US-09-925-299-791
15	27	90.0	345	14	US-10-156-761-10629

16	27	90.0	389	14	US-10-106-698-4653	Sequence 4653, Ap
17	27	90.0	435	15	US-10-369-493-13783	Sequence 13783, A
18	27	90.0	450	15	US-10-369-493-1266	Sequence 1266, Ap
19	27	90.0	450	15	US-10-369-493-20332	Sequence 20332, A
20	27	90.0	450	15	US-10-369-493-21647	Sequence 21647, A
21	27	90.0	510	14	US-10-128-714-3191	Sequence 3191, Ap
22	27	90.0	529	15	US-10-094-749-1678	Sequence 1678, Ap
23	27	90.0	613	9	US-09-738-626-4899	Sequence 4899, Ap
24	27	90.0	622	15	US-10-369-493-1366	Sequence 1366, Ap
25	27	90.0	632	14	US-10-128-714-8191	Sequence 8191, Ap
26	27	90.0	645	9	US-09-815-242-5823	Sequence 5823, Ap
27	27	90.0	727	9	US-09-801-368-296	Sequence 296, App
28	27	90.0	880	10	US-09-893-519A-36	Sequence 36, Appl
29	27	90.0	961	15	US-10-231-913-102	Sequence 102, App
30	27	90.0	1111	9	US-09-815-242-12955	Sequence 12955, A
31	27	90.0	1328	15	US-10-369-493-18867	Sequence 18867, A
32	27	90.0	1328	15	US-10-369-493-20000	Sequence 20000, A
33	27	90.0	2133	14	US-10-187-319-37	Sequence 37, Appl
34	27	90.0	2133	14	US-10-131-510A-37	Sequence 37, Appl
35	26	86.7	120	10	US-09-809-920-6	Sequence 6, Appli
36	26	86.7	265	15	US-10-369-493-7827	Sequence 7827, Ap
37	26	86.7	305	14	US-10-128-714-3145	Sequence 3145, Ap
38	26	86.7	315	14	US-10-128-714-8145	Sequence 8145, Ap
39	26	86.7	370	15	US-10-259-194A-44	Sequence 44, Appl
40	26	86.7	512	15	US-10-259-194A-224	Sequence 224, App
41	26	86.7	549	13	US-10-044-205A-14	Sequence 14, Appl
42	26	86.7	557	13	US-10-044-205A-13	Sequence 13, Appl
43	26	86.7	645	9	US-09-764-868-625	Sequence 625, App
44	26	86.7	663	14	US-10-102-806-654	Sequence 654, App
45	26	86.7	672	15	US-10-094-749-1885	Sequence 1885, Ap

ALIGNMENTS

RESULT 1
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942.024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Query Match	100.0%	Score 30;	DB 10;	Length 206;
Best Local Similarity	100.0%	Pred. No. 1.1e+02;		
Matches	6;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
Qy	1 EEMQRR 6			
Db	12 EEMQRR 17			
RESULT 2				
US-09-942-024-7				
; Sequence 7, Application US/09942024				
; Publication No. US20030143650A1				
; GENERAL INFORMATION:				
; APPLICANT: Steward, Lance E.				
; APPLICANT: Fernandez-Salas, Ester				
; APPLICANT: Aoki, Kei Roger				

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 3
US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-12

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 4
US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester

; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2

Query Match 100.0%; Score 30; DB 10; Length 206;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 5
US-09-942-098-7
; Sequence 7, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-098-7

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 6
US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 7
US-09-942-024-16
; Sequence 16, Application US/09942024
; Publication No. US20030143650A1

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; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-024-16

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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QY      1 EEMQRR 6
Db      12 EEMQRR 17

RESULT 8
US-09-942-098-16
; Sequence 16, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
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; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-098-16

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      12 EEMQRR 17

RESULT 9
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; Publication No. US20020164735A1
; GENERAL INFORMATION:
; APPLICANT: OLSON, ERIC N.
; APPLICANT: WANG, DA-ZHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC
; FILE REFERENCE: UTSD:695US
; CURRENT APPLICATION NUMBER: US/10/029,217A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/257,761
; PRIOR FILING DATE: 2000-12-21
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; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 35
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; ORGANISM: Mus musculus
US-10-029-217A-21

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Best Local Similarity 83.3%; Pred. No. 78;
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Db      11 EELQRR 16

RESULT 10
US-10-082-828A-255
; Sequence 255, Application US/10082828A
; Publication No. US20030175715A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Heirve
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and P
; FILE REFERENCE: DEX-0247
; CURRENT APPLICATION NUMBER: US/10/082,828A
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/243,805
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 255
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-828A-255

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Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEMQRR 6
Db      46 EEMQRR 51

RESULT 11
US-09-925-300-1287
; Sequence 1287, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1287
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

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; LOCATION: (193)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (207)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (210)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (211)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1287
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Query Match          90.0%; Score 27; DB 9; Length 214;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EEMQRR 6
      |||:|
Db      65 EELQRR 70
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RESULT 12

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US-10-029-386-33812
; Sequence 33812, Application US/10029386
; Publication No. US20030194704A1
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; GENERAL INFORMATION:
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; APPLICANT: Penn, Sharon G.
```

```
; APPLICANT: Hanzel, David K.
```

```
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
```

```
; FILE REFERENCE: AEOMICA-X-2
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; CURRENT APPLICATION NUMBER: US/10/029,386
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; CURRENT FILING DATE: 2001-12-20
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; NUMBER OF SEQ ID NOS: 34288
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; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
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; SEQ ID NO 33812
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; LENGTH: 240
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; TYPE: PRT
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; ORGANISM: Homo sapiens
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; FEATURE:
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; OTHER INFORMATION: MAP TO AL136001.1
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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.37
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; OTHER INFORMATION: SWISSPROT HIT: Q9JL04, EVALUATE 1.20e+00
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US-10-029-386-33812
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Query Match          90.0%; Score 27; DB 14; Length 240;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EEMQRR 6
      ||||:|
Db     229 EEMQRR 234
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RESULT 13

```
US-09-925-299-791
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```
; Sequence 791, Application US/09925299
```

```
; Patent No. US20020055627A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Rosen et al.
```

```
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
```

```
; FILE REFERENCE: PA102
```

```
; CURRENT APPLICATION NUMBER: US/09/925,299
```

```
; CURRENT FILING DATE: 2001-08-10
```

```
; PRIOR APPLICATION NUMBER: PCT/US00/05883
```

```
; PRIOR FILING DATE: 2000-03-08
```

```
; PRIOR APPLICATION NUMBER: 60/124,270
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; PRIOR FILING DATE: 1999-03-12
```

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; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 791
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-791
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Query Match          90.0%; Score 27; DB 9; Length 245;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EEMQRR 6
      |||:|
Db     136 EELQRR 141
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RESULT 14

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US-09-925-299-791
```

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; Sequence 791, Application US/09925299
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```
; Publication No. US20030040617A9
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; GENERAL INFORMATION:
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```
; APPLICANT: Rosen et al.
```

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; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
```

```
; FILE REFERENCE: PA102
```

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; CURRENT APPLICATION NUMBER: US/09/925,299
```

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; CURRENT FILING DATE: 2001-08-10
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; PRIOR APPLICATION NUMBER: PCT/US00/05883
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; PRIOR FILING DATE: 2000-03-08
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; PRIOR APPLICATION NUMBER: 60/124,270
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; NUMBER OF SEQ ID NOS: 1556
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; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 791
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; LENGTH: 245
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; TYPE: PRT
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; ORGANISM: Homo sapiens
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US-09-925-299-791
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Query Match          90.0%; Score 27; DB 10; Length 245;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EEMQRR 6
      |||:|
Db     136 EELQRR 141
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RESULT 15

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US-10-156-761-10629
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; Sequence 10629, Application US/10156761
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; Publication No. US20030119018A1
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```
; GENERAL INFORMATION:
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```
; APPLICANT: OMURA, SATOSHI
```

```
; APPLICANT: IKEDA, HARUO
```

```
; APPLICANT: ISHIKAWA, JUN
```

```
; APPLICANT: HORIKAWA, HIROSHI
```

```
; APPLICANT: SHIBA, TADAYOSHI
```

```
; APPLICANT: SAKAKI, YOSHIYUKI
```

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; APPLICANT: HATTORI, MASAHIRA
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; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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; FILE REFERENCE: 249-262
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; CURRENT APPLICATION NUMBER: US/10/156,761
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; CURRENT FILING DATE: 2002-05-29
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; PRIOR APPLICATION NUMBER: JP 2001-204089
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; PRIOR FILING DATE: 2001-05-30
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; PRIOR APPLICATION NUMBER: JP 2001-272697
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; PRIOR FILING DATE: 2001-08-02
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; NUMBER OF SEQ ID NOS: 15109
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; SEQ ID NO 10629
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; LENGTH: 345
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; TYPE: PRT
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; ORGANISM: Streptomyces avermitilis
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US-10-156-761-10629

Query Match 90.0%; Score 27; DB 14; Length 345;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||:|
Db 214 EEMERR 219

Search completed: March 4, 2004, 08:30:59
Job time : 17.3684 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 08:26:00 ; Search time 10.1053 Seconds
(without alignments)
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Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	100.0	68	4	US-09-621-976-7614 Sequence 7614, Ap
2	30	100.0	206	1	US-08-393-985-18 Sequence 18, Appl
3	30	100.0	206	3	US-08-819-286-1 Sequence 1, Appli
4	27	90.0	200	4	US-09-252-991A-23347 Sequence 23347, A
5	27	90.0	231	4	US-09-252-991A-27366 Sequence 27366, A
6	27	90.0	314	4	US-09-543-681A-5695 Sequence 5695, Ap
7	27	90.0	375	1	US-07-803-622E-7 Sequence 7, Appli
8	27	90.0	375	1	US-07-803-622E-9 Sequence 9, Appli
9	27	90.0	534	4	US-09-107-532A-6549 Sequence 6549, Ap
10	27	90.0	612	3	US-09-318-794A-5 Sequence 5, Appli
11	27	90.0	739	1	US-07-803-622E-2 Sequence 2, Appli
12	27	90.0	868	1	US-07-864-004B-6 Sequence 6, Appli
13	27	90.0	868	1	US-08-251-937A-6 Sequence 6, Appli
14	27	90.0	868	1	US-08-212-133A-3 Sequence 3, Appli
15	27	90.0	914	4	US-09-437-054A-8 Sequence 8, Appli
16	27	90.0	1090	5	PCT-US93-03275-6 Sequence 6, Appli
17	27	90.0	2115	3	US-09-324-867-5 Sequence 5, Appli
18	27	90.0	2133	2	US-08-670-707A-37 Sequence 37, Appl
19	27	90.0	2133	3	US-09-037-601-37 Sequence 37, Appl
20	27	90.0	2133	4	US-09-315-179-37 Sequence 37, Appl
21	27	90.0	2133	4	US-09-523-656-30 Sequence 30, Appl
22	26	86.7	253	4	US-09-252-991A-31497 Sequence 31497, A
23	26	86.7	362	4	US-09-107-532A-7093 Sequence 7093, Ap
24	26	86.7	363	4	US-09-252-991A-32850 Sequence 32850, A
25	26	86.7	496	4	US-09-252-991A-20207 Sequence 20207, A
26	26	86.7	496	4	US-09-540-236-3821 Sequence 3821, Ap
27	26	86.7	728	3	US-08-915-337-2 Sequence 2, Appli

28	26	86.7	1251	4	US-09-698-286A-9 Sequence 9, Appli
29	26	86.7	1375	4	US-09-722-139-2 Sequence 2, Appli
30	26	86.7	1375	4	US-09-721-832-2 Sequence 2, Appli
31	26	86.7	1375	4	US-09-721-689-2 Sequence 2, Appli
32	25	83.3	98	4	US-09-489-039A-7345 Sequence 7345, Ap
33	25	83.3	108	4	US-09-328-352-5930 Sequence 5930, Ap
34	25	83.3	203	4	US-09-489-039A-7593 Sequence 7593, Ap
35	25	83.3	235	2	US-09-141-135-2 Sequence 2, Appli
36	25	83.3	235	4	US-09-533-029-98 Sequence 98, Appl
37	25	83.3	255	4	US-09-364-230-34 Sequence 34, Appl
38	25	83.3	277	4	US-09-489-039A-7505 Sequence 7505, Ap
39	25	83.3	341	4	US-09-252-991A-27327 Sequence 27327, A
40	25	83.3	346	3	US-09-049-672A-28 Sequence 28, Appl
41	25	83.3	378	4	US-09-107-532A-6500 Sequence 6500, Ap
42	25	83.3	392	4	US-09-600-099-6 Sequence 6, Appli
43	25	83.3	415	4	US-09-252-991A-30511 Sequence 30511, A
44	25	83.3	452	4	US-09-277-262-8 Sequence 8, Appli
45	25	83.3	471	3	US-08-866-928B-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-7614
; Sequence 7614, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7614
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7614

Query Match 100.0%; Score 30; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 2
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18

Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 3
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1

Query Match 100.0%; Score 30; DB 3; Length 206;

Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 4
US-09-252-991A-23347
; Sequence 23347, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23347
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23347

Query Match 90.0%; Score 27; DB 4; Length 200;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 86 EELQRR 91

RESULT 5
US-09-252-991A-27366
; Sequence 27366, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27366
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27366

Query Match 90.0%; Score 27; DB 4; Length 231;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 203 EELQRR 208

RESULT 6
US-09-543-681A-5695
; Sequence 5695, Application US/09543681A

Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIORITY FILING DATE: 2000-04-05
PRIORITY FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5695
LENGTH: 314
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5695

Query Match 90.0%; Score 27; DB 4; Length 314;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 135 EELQRR 140

RESULT 7
US-07-803-622E-7
; Sequence 7, Application US/07803622E
; Patent No. 5525497
; GENERAL INFORMATION:
; APPLICANT: Keller, Walter
; APPLICANT: Lingner, Joachim
; APPLICANT: Martin, Georges
; APPLICANT: Wahle, Elmar
; TITLE OF INVENTION: RECOMBINANT POLY(A) POLYMERASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803,622E
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 195/296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-803-622E-7

Query Match 90.0%; Score 27; DB 1; Length 375;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 135 EELQRR 140

RESULT 8
US-07-803-622E-8
; Sequence 8, Application US/07803622E
; Patent No. 5525497
; GENERAL INFORMATION:
; APPLICANT: Keller, Walter
; APPLICANT: Lingner, Joachim
; APPLICANT: Martin, Georges
; APPLICANT: Wahle, Elmar
; TITLE OF INVENTION: RECOMBINANT POLY(A) POLYMERASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803,622E
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 195/296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-803-622E-8

Query Match 90.0%; Score 27; DB 1; Length 375;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 56 EELQRR 61

RESULT 9
US-09-107-532A-6549
; Sequence 9, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

Query Match 90.0%; Score 27; DB 1; Length 375;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 56 EELQRR 61

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6549:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...534
SEQUENCE DESCRIPTION: SEQ ID NO: 6549:
US-09-107-532A-6549

Query Match 90.0%; Score 27; DB 4; Length 534;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 39 EEMERR 44

RESULT 10
US-09-318-794A-5
Sequence 5, Application US/09318794A
Patent No. 6177264
GENERAL INFORMATION:
APPLICANT: DEGUSSA AKTIENGESSELLSCHAFT
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
FILE REFERENCE: eggeling
CURRENT APPLICATION NUMBER: US/09/318,794A
PRIOR FILING DATE: 1999-05-26
PRIOR FILING DATE: DE 198 55 312.9
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 612
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-318-794A-5

Query Match 90.0%; Score 27; DB 3; Length 612;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 564 EELQRR 569

RESULT 11
US-07-803-622E-2
Sequence 2, Application US/07803622E
Patent No. 5525497
GENERAL INFORMATION:
APPLICANT: Keller, Walter
APPLICANT: Lingner, Joachim
APPLICANT: Martin, Georges
APPLICANT: Wahle, Elmar
TITLE OF INVENTION: RECOMBINANT POLY(A) POLYMERASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/803,622E
FILING DATE: 27-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 195/296
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-489-1600
TELEFAX: 213-955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 739 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-803-622E-2

Query Match 90.0%; Score 27; DB 1; Length 739;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 56 EELQRR 61

RESULT 12
US-07-864-004B-6
Sequence 6, Application US/07864004B
Patent No. 5364771
GENERAL INFORMATION:
APPLICANT: Lollar, John S.
APPLICANT: Runge, Marshall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/864,004B
;; FILING DATE: 07 APRIL 1992
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: EMU106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 404-815-6508
;; TELEFAX: 404-815-6555
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 868 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Porcine
US-07-864-004B-6

Query Match 90.0%; Score 27; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||:|
Db 418 EEMERR 423

RESULT 13
US-08-251-937A-6
; Sequence 6, Application US/08251937A
; Patent No. 5583209
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; APPLICANT: Runge, Marschall S.
; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/251,937A
; FILING DATE: 31-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pratt, John S.
; REGISTRATION NUMBER: 29,476
; REFERENCE/DOCKET NUMBER: EMU106DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6367
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Porcine
US-08-251-937A-6

Query Match 90.0%; Score 27; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||:|
Db 418 EEMERR 423

RESULT 14
US-08-212-133A-3
; Sequence 3, Application US/08212133A
; Patent No. 5663060
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; APPLICANT: Runge, Marschall S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,133A
; FILING DATE: March 11, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU/76677
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-572-6508
; TELEFAX: 404-572-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Porcine
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..868
; OTHER INFORMATION: /note= "Predicted amino acid
; OTHER INFORMATION: sequence of the B and part of the A2 domains of
; OTHER INFORMATION: porcine factor VIII."

US-08-212-133A-3

Query Match 90.0%; Score 27; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
Db 418 EEMERR 423

RESULT 15

US-09-437-054A-8
; Sequence 8, Application US/09437054A
; Patent No. 6316698
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
; FILE REFERENCE: BB1273 US NA
; CURRENT APPLICATION NUMBER: US/09/437,054A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/107,909
; PRIOR FILING DATE: 1998-No. 6316698ember-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Glycine max
US-09-437-054A-8

Query Match 90.0%; Score 27; DB 4; Length 914;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
Db 413 EEMQRR 418

Search completed: March 4, 2004, 08:31:45
Job time : 11.1053 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 31.8947 Seconds
(without alignments)
53.153 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	6	AAB15582	Aab15582 Human SNA
2	30	100.0	13	AAB15583	Aab15583 Human SNA
3	30	100.0	64	AAG00764	Aag00764 Human sec
4	30	100.0	82	AAB15581	Aab15581 Human SNA
5	30	100.0	93	ABU43453	Abu43453 Protein e
6	30	100.0	106	AAG03825	Aag03825 Human sec
7	30	100.0	106	AAG03826	Aag03826 Human sec
8	30	100.0	198	AAU00255	Aau00255 Synaptoso
9	30	100.0	199	AAU00263	Aau00263 Synaptoso
10	30	100.0	200	AAU00264	Aau00264 Synaptoso
11	30	100.0	201	AAU02637	Aau02637 Synaptoso
12	30	100.0	202	AAU00265	Aau00265 Synaptoso
13	30	100.0	203	AAU02636	Aau02636 Synaptoso
14	30	100.0	206	AAW30103	Aaw30103 Synaptoso
15	30	100.0	206	AAW43426	Aaw43426 Mouse syn
16	30	100.0	206	AAW79198	Aaw79198 Mouse SNA
17	30	100.0	206	AAU00256	Aau00256 Synaptoso
18	30	100.0	206	AAU00261	Aau00261 Synaptoso
19	30	100.0	206	AAU00246	Aau00246 Synaptoso
20	30	100.0	206	AAU00253	Aau00253 SNARE hom
21	30	100.0	206	AAU02171	Aau02171 Synaptoso
22	30	100.0	206	AAU00266	Aau00266 Synaptoso
23	30	100.0	206	AAU02640	Aau02640 Synaptoso
24	30	100.0	206	AAU00258	Aau00258 Synaptoso
25	30	100.0	206	AAU00262	Aau00262 Synaptoso

26	30	100.0	206	4	AAU00259	Aau00259 Synaptoso
27	30	100.0	206	4	AAU00252	Aau00252 SNARE hom
28	30	100.0	206	4	AAU00260	Aau00260 Synaptoso
29	30	100.0	206	4	AAU02638	Aau02638 Synaptoso
30	30	100.0	206	4	AAU02639	Aau02639 Synaptoso
31	30	100.0	206	4	AAU00257	Aau00257 Synaptoso
32	30	100.0	206	6	AAE36662	Aae36662 Human SNA
33	30	100.0	206	6	AAE36667	Aae36667 Rat VAMP-
34	30	100.0	206	7	ADE54280	Ades4280 Rat Prote
35	30	100.0	206	7	ADE54288	Ades4288 Rat Prote
36	30	100.0	206	7	ADE54276	Ades4276 Rat Prote
37	30	100.0	206	7	ADE54290	Ades4290 Human Pro
38	30	100.0	206	7	ADE54282	Ades4282 Rat Prote
39	30	100.0	206	7	ADE54274	Ades4274 Rat Prote
40	30	100.0	206	7	ADE54286	Ades4286 Human Pro
41	30	100.0	206	7	ADE54284	Ades4284 Rat Prote
42	30	100.0	206	7	ADE54272	Ades4272 Rat Prote
43	30	100.0	206	7	ADE54278	Ades4278 Rat Prote
44	30	100.0	537	4	ABB59734	Abb59734 Drosophil
45	27	90.0	35	5	ABG70819	Abg70819 Mouse myo

ALIGNMENTS

RESULT 1
AAB15582
ID AAB15582 standard; peptide; 6 AA.
XX
AC AAB15582;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human SNAP-25 N-terminal peptide #2.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN WO200064932-A1.
XX
PD 02-NOV-2000.
XX
PF 18-FEB-2000; 2000WO-ES000058.
XX
PR 23-APR-1999; 99ES-00000844.
XX
(LIPO-) LIPOTEC SA.
Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
Viniestra Bover S, Gutierrez Perez LM, Carbonell Castell T;
Perez Paya E;
WPI; 2001-007091/01.
New peptides containing amino acid sequences from known proteins for
treatment of neurological disorders.
Claim 9; Page 32; 40pp; Spanish.
The invention relates to new peptides comprising 3-30 contiguous amino
acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
protein 25). The peptides AAB15581-B15586 represent examples of the
peptides of the invention. The peptides have neuronal exocytosis
inhibitory activity and are used for treatment of facial wrinkles and
asymmetry and pathological neuronal exocytosis-mediated pathological
disorders and alterations manifested e.g. by spasms and neurological and
neurodegenerative disorders
Sequence 6 AA;
SQ

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Query Match      100.0%; Score 30; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 1 EEMQRR 6

RESULT 2
AAB15583
ID AAB15583 standard; peptide; 13 AA.
XX AAB15583;
AC AAB15583;
XX 02-MAR-2001 (first entry)
XX Human SNAP-25 N-terminal peptide #3.
DE Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
XX SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX Homo sapiens.
OS Homo sapiens.
XX WO200064932-A1.
PN WO200064932-A1.
XX 02-NOV-2000.
XX 18-FEB-2000; 2000WO-ES000058.
PF 23-APR-1999; 99ES-00000844.
PR (LIPO-) LIPOTEC SA.
XX Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;
XX WPI; 2001-007091/01.
DR New peptides containing amino acid sequences from known proteins for
XX treatment of neurological disorders.
PT Claim 9; Page 32; 40pp; Spanish.
PS The invention relates to new peptides comprising 3-30 contiguous amino
XX acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AAB15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
CC neurodegenerative disorders
XX Sequence 13 AA;
SQ Query Match      100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 3 EEMQRR 8

RESULT 3
AAG00764
ID AAG00764 standard; protein; 64 AA.
XX AAG00764;
AC AAG00764;
```

```
XX 06-OCT-2000 (first entry)
DT Human secreted protein, SEQ ID NO: 4845.
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX Homo sapiens.
OS Homo sapiens.
XX EP1033401-A2.
PN 06-SEP-2000.
XX 21-FEB-2000; 2000EP-00200610.
PF 26-FEB-1999; 99US-0122487P.
XX (GEST ) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI; 2000-500381/45.
XX N-PSDB; AAC00770.
DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX Claim 13; SEQ ID NO 4845; 71pp + Sequence Listing; English.
XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX SQ Sequence 64 AA;
Query Match      100.0%; Score 30; DB 3; Length 64;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 4
AAB15581
ID AAB15581 standard; peptide; 82 AA.
XX AAB15581;
AC AAB15581;
XX 02-MAR-2001 (first entry)
XX Human SNAP-25 N-terminal peptide #1.
DE Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
XX SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX Homo sapiens.
OS Homo sapiens.
XX WO200064932-A1.
```

XX PD 02-NOV-2000.
 XX PF 18-FEB-2000; 2000WO-ES000058.
 XX PR 23-APR-1999; 99ES-00000844.
 XX PA (LIPO-) LIPOTEC SA.
 XX PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
 PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
 PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
 PI Perez Paya E;
 XX DR WPI; 2001-007091/01.
 XX PT New peptides containing amino acid sequences from known proteins for
 PT treatment of neurological disorders.
 XX PS Claim 1; Page 31; 40pp; Spanish.
 XX CC The invention relates to new peptides comprising 3-30 contiguous amino
 CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
 CC protein 25). The peptides AAB15581-B15586 represent examples of the
 CC peptides of the invention. The peptides have neuronal exocytosis
 CC inhibitory activity and are used for treatment of facial wrinkles and
 CC asymmetry and pathological neuronal exocytosis-mediated pathological
 CC disorders and alterations manifested e.g. by spasms and neurological and
 CC neurodegenerative disorders
 XX SQ Sequence 82 AA;
 Query Match 100.0%; Score 30; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EEMQRR 6
 Db |||||
 11 EEMQRR 16
 RESULT 5
 ABU43453
 ID ABU43453 standard; protein; 93 AA.
 XX AC ABU43453;
 XX DT 19-JUN-2003 (first entry)
 XX DE Protein encoded by Prokaryotic essential gene #28980.
 XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX OS Staphylococcus haemolyticus.
 XX PN WO200277183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 XX PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.

DR N-PSDB; ACA47323.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 25; SEQ ID NO 71377; 1766pp; English.
 XX CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 93 AA;
 Query Match 100.0%; Score 30; DB 6; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EEMQRR 6
 Db |||||
 24 EEMQRR 29
 RESULT 6
 AAG03825
 ID AAG03825 standard; protein; 106 AA.
 XX AC AAG03825;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 7906.
 XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.

XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX DR WPI; 2000-500381/45.
 XX DR N-PSDB; AAC03831.
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX PS Claim 13; SEQ ID NO 7906; 71pp + Sequence Listing; English.
 XX CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX SQ Sequence 106 AA;
 Query Match 100.0%; Score 30; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 12 EEMQRR 17
 RESULT 7
 AAG03826
 ID AAG03826 standard; protein; 106 AA.
 XX AC AAG03826;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 7907.
 XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.
 XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX DR WPI; 2000-500381/45.
 XX DR N-PSDB; AAC03832.
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX

PS Claim 13; SEQ ID NO 7907; 71pp + Sequence Listing; English.
 XX CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX SQ Sequence 106 AA;
 Query Match 100.0%; Score 30; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 12 EEMQRR 17
 RESULT 8
 AAU00255
 ID AAU00255 standard; protein; 198 AA.
 XX AC AAU00255;
 XX DT 12-SEP-2001 (first entry)
 XX DE Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.
 XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX OS Mus sp.
 OS Synthetic.
 XX PN WO200118038-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX DR WPI; 2001-226739/23.
 XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new
 CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the

CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state. Note: The present sequence is
 CC not shown in the specification but is derived from the mouse SNAP-25
 CC sequence given in figure 8 (see AAU00246)
 XX
 SQ Sequence 198 AA;

Query Match 100.0%; Score 30; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 DB 12 EEMQRR 17

RESULT 9
 AAU00263
 ID AAU00263 standard; protein; 199 AA.

XX AAU00263;

DT 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant 1-199(R198T).

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-199(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 199 AA;

Query Match 100.0%; Score 30; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 DB 12 EEMQRR 17

RESULT 10
 AAU00264

ID AAU00264 standard; protein; 200 AA.

XX AAU00264;

DT 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant 1-200(R198T).

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX
PT Treating a patient suffering from poisoning or at risk of poisoning by a
PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.
XX
PS Example 1; Page; 131pp; English.
XX
CC The sequence represents the amino acid sequence of synaptosomal-
CC associated protein, SNAP25, mutant 1-200(R198T), used in a new method of
CC treating a patient suffering from poisoning or at risk of poisoning by a
CC clostridial toxin, comprising supplying a SNARE (soluble (N-
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
CC a cell of the patient, where the SNARE is resistant to proteolysis by the
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
CC capable of performing SNARE-dependent exocytosis, comprises supplying a
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
CC or a recombinant polynucleotide encoding the SNARE is useful in the
CC manufacture of a medicament for the treatment of a patient suffering from
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
CC botulism or tetanus. The fragment, variant, fusion or derivative of a
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
CC either of these SNARE polypeptides are useful in the manufacture of
CC medicament for the treatment of a patient in need of inhibition of SNARE-
CC dependent exocytosis from a cell capable of performing SNARE-dependent
CC exocytosis. The method of treatment is relatively fast, thus alleviating
CC the symptoms when most severe and taking the patient out of critical
CC state. Note: The present sequence is not shown in the specification but
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
CC AAU00246)
XX
SQ Sequence 200 AA;

Query Match 100.0%; Score 30; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db ||||| 12 EEMQRR 17

RESULT 11
AAU02637
ID AAU02637 standard; protein; 201 AA.
XX
AC AAU02637;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).
XX
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 198
FT /note= "Wild-type Arg substituted by Thr"
XX
PN WO200118038-A2.
XX
PD 15-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-GB003196.
XX

PR 20-AUG-1999; 99US-0149993P.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
XX
DR WPI; 2001-226739/23.
XX
PT Treating a patient suffering from poisoning or at risk of poisoning by a
PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.
XX
PS Example 1; Page; 131pp; English.
XX
CC The sequence represents the amino acid sequence of synaptosomal-
CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
CC treating a patient suffering from poisoning or at risk of poisoning by a
CC clostridial toxin, comprising supplying a SNARE (soluble (N-
CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
CC a cell of the patient, where the SNARE is resistant to proteolysis by the
CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
CC capable of performing SNARE-dependent exocytosis, comprises supplying a
CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
CC or a recombinant polynucleotide encoding the SNARE is useful in the
CC manufacture of a medicament for the treatment of a patient suffering from
CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
CC botulism or tetanus. The fragment, variant, fusion or derivative of a
CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
CC either of these SNARE polypeptides are useful in the manufacture of
CC medicament for the treatment of a patient in need of inhibition of SNARE-
CC dependent exocytosis from a cell capable of performing SNARE-dependent
CC exocytosis. The method of treatment is relatively fast, thus alleviating
CC the symptoms when most severe and taking the patient out of critical
CC state. Note: The present sequence is not shown in the specification but
CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
CC AAU00246)
XX
SQ Sequence 201 AA;

Query Match 100.0%; Score 30; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db ||||| 12 EEMQRR 17

RESULT 12
AAU00265
ID AAU00265 standard; protein; 202 AA.
XX
AC AAU00265;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synaptosomal-associated protein, SNAP25, mutant 1-202(R198T).
XX
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
KW synaptosomal-associated protein; mouse; mutant; mutein;
KW N-ethylmaleimide-sensitive fusion protein;
KW soluble NSF-attachment protein receptor.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 198
FT /note= "Wild-type Arg substituted by Thr"
FT

XX PN WO200118038-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX DR WPI; 2001-226739/23.
 XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
 XX PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX PT resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 XX CC associated protein, SNAP25, mutant 1-202(R198T), used in a new method of
 XX CC treating a patient suffering from poisoning or at risk of poisoning by a
 XX CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 XX CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX CC or a recombinant polynucleotide encoding the SNARE is useful in the
 XX CC manufacture of a medicament for the treatment of a patient suffering from
 XX CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX CC medicament for the treatment of a patient in need of inhibition of SNARE-
 XX CC dependent exocytosis from a cell capable of performing SNARE-dependent
 XX CC exocytosis. The method of treatment is relatively fast, thus alleviating
 XX CC the symptoms when most severe and taking the patient out of critical
 XX CC state. Note: The present sequence is not shown in the specification but
 XX CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX CC AAU00246)
 XX SQ Sequence 202 AA;
 Query Match 100.0%; Score 30; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 12 EEMQRR 17
 RESULT 13
 AAU02636
 ID AAU02636 standard; protein; 203 AA.
 XX AC AAU02636;
 XX DT 12-SEP-2001 (first entry)
 XX DE Synaptosomal-associated protein, SNAP25, mutant 1-203(R198T).
 XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 XX KW synaptosomal-associated protein; mouse; mutant; mutein;
 XX KW N-ethylmaleimide-sensitive fusion protein;
 XX KW soluble NSF-attachment protein receptor.

XX OS Mus sp.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 198
 XX FT /note= "Wild-type Arg substituted by Thr"
 XX PN WO200118038-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX DR WPI; 2001-226739/23.
 XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
 XX PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX PT resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 XX CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 XX CC treating a patient suffering from poisoning or at risk of poisoning by a
 XX CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 XX CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX CC or a recombinant polynucleotide encoding the SNARE is useful in the
 XX CC manufacture of a medicament for the treatment of a patient suffering from
 XX CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX CC either of these SNARE polypeptides are useful in the manufacture of
 XX CC medicament for the treatment of a patient in need of inhibition of SNARE-
 XX CC dependent exocytosis from a cell capable of performing SNARE-dependent
 XX CC exocytosis. The method of treatment is relatively fast, thus alleviating
 XX CC the symptoms when most severe and taking the patient out of critical
 XX CC state. Note: The present sequence is not shown in the specification but
 XX CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX CC AAU00246)
 XX SQ Sequence 203 AA;
 Query Match 100.0%; Score 30; DB 4; Length 203;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 12 EEMQRR 17
 RESULT 14
 AAU030103
 ID AAU030103 standard; peptide; 206 AA.
 XX AC AAU030103;
 XX DT 06-APR-1998 (first entry)
 XX

DE Synaptosomal associated protein.
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX
 OS Homo sapiens.
 XX
 PN WO9734620-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US004393.
 XX
 PR 18-MAR-1996; 96US-0013599P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Montal M;
 XX
 DR WPI; 1997-479986/44.
 XX
 PT Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neuro:transmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 XX
 PS Disclosure; Page 27-28; 61pp; English.
 XX
 CC This sequence represents the human 25 kD synaptosomal associated protein
 CC (SNAP-25), which is an inhibitory agent of the invention. The agents of
 CC the invention inhibit secretion of neurotransmitter from neuronal cells
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20
 CC amino acids (aa) all of which correspond substantially to any one of
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
 CC catecholamine secretion from bovine chromaffin cells at a concentration
 CC of 10 microM, especially 0.25 microM, or less. (I) are used, as a
 CC replacement for Clostridium toxin, to inhibit release of
 CC neurotransmitters from synaptic vesicles, specifically for reducing
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
 CC intracellular distribution of (I). Compounds for delivering the drug to
 CC neural cells provide targeted drug delivery, e.g. of substance P to brain
 CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
 CC toxic or immunogenic and are more readily available. Their therapeutic
 CC effect lasts for several days or weeks, so lower doses or less frequent
 CC treatments are required
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 30; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db |||||
 12 EEMQRR 17
 RESULT 15
 AAW43426
 ID AAW43426 standard; protein; 206 AA.
 XX
 AC AAW43426;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Mouse synaptosomal-associated protein-25.
 XX
 KW Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;
 KW neurotransmitter; presynaptic membrane; central nervous system; tumour;
 KW neurodegenerative disease; hormonal disorder; immunological disorder.
 OS Mus sp.

XX US5693476-A.
 PN
 XX 02-DEC-1997.
 PD
 XX 24-FEB-1995; 95US-00393985.
 PF
 XX 24-FEB-1995; 95US-00393985.
 PR
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX Scheller RH;
 PI
 XX WPI; 1998-031743/03.
 DR N-PSDB; AAV01554.
 XX
 PT Screening assay for modulators of syntaxin binding - using peptide
 PT comprising binding site of syntaxin, for identifying drugs useful for
 PT treating CNS disorders, neuro-degenerative diseases, etc.
 XX
 PS Disclosure; Col 67-72; 57pp; English.
 XX
 CC This amino acid sequence represents the mouse synaptosomal-associated
 CC protein of 25 kD (SNAP-25). The invention relates to a method for
 CC identifying a compound capable of affecting the binding of a syntaxin-
 CC binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to
 CC syntaxin. The method comprises measuring the effect of the test compound
 CC on the extent of binding between the SBP and the SBP-binding site on
 CC syntaxin. The method can be used for identifying drugs capable of
 CC inhibiting or stimulating neurotransmitter release at the active zones of
 CC presynaptic membranes, which may be useful for treating CNS disorders,
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or
 CC immunological disorders or tumours
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 30; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db |||||
 12 EEMQRR 17
 Search completed: March 4, 2004, 08:27:49
 Job time : 32.8947 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:04:11 ; Search time 35.5135 Seconds
(without alignments)
159.920 Million cell updates/sec

Title: US-10-030-485A-5
Perfect score: 89
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	124	13	O93578
2	89	100.0	143	6	Q9GM34
3	80	89.9	203	13	O93579
4	80	89.9	206	13	Q8AXM2
5	80	89.9	206	13	Q8AXM1
6	70	78.7	204	13	Q8JIS7
7	70	78.7	214	13	Q7ZVE4
8	65	73.0	212	5	Q8T3S4
9	59	66.3	210	11	O35620
10	59	66.3	210	11	O70377
11	59	66.3	210	11	O09044
12	59	66.3	221	11	O9D313
13	50	56.2	90	5	O96578
14	50	56.2	125	5	O96576
15	50	56.2	207	5	O62414
16	48	53.9	1202	10	Q8LMQ4

17	47	52.8	659	10	Q41074
18	46	51.7	240	2	Q9RGE7
19	45	50.6	1138	5	Q22276
20	44	49.4	191	17	Q8ZY72
21	44	49.4	212	5	O44419
22	44	49.4	212	5	O76338
23	44	49.4	220	5	O869G6
24	44	49.4	584	2	Q9KH13
25	44	49.4	776	16	Q89QI8
26	44	49.4	1297	5	Q8IC22
27	43	48.3	395	4	Q96LN4
28	43	48.3	401	16	Q9PIU7
29	43	48.3	480	5	Q17621
30	43	48.3	623	4	Q8NCN6
31	43	48.3	1036	5	Q8I950
32	42.5	47.8	524	3	Q9P865
33	42	47.2	86	15	P89733
34	42	47.2	173	16	Q45938
35	42	47.2	207	5	Q8IAE1
36	42	47.2	207	5	Q8IAE0
37	42	47.2	212	5	O01389
38	42	47.2	304	2	Q9K580
39	42	47.2	334	6	Q95JR9
40	42	47.2	403	16	Q7WJ36
41	42	47.2	419	2	Q9ZFG6
42	42	47.2	447	2	Q9AGH6
43	42	47.2	551	6	Q95JV6
44	42	47.2	658	5	Q76180
45	42	47.2	659	5	Q8I866

ALIGNMENTS

RESULT 1

O93578 ID O93578 PRELIMINARY; PRT; 124 AA.
AC O93578;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN SNAP25A OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99057281; PubMed=9843147;
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573(1998).
DR ENBL; AF091593; AAC64289.1; -.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
FT NON TER 1
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBB33D958C CRC64;

Query Match 100.0%; Score 89; DB 13; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RIMEKADSNKTRIDEANQ 18

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Db 98 RIMEKADSNKTRIDEANQ 115
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RESULT 2
Q9GM34 Q9GM34 PRELIMINARY; PRT; 143 AA.
AC Q9GM34;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049852; BAB16738.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
KW Hypothetical protein.
SQ SEQUENCE 143 AA; 16043 MW; D625DBAA0893FE0 CRC64;

Query Match 100.0%; Score 89; DB 6; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||||
Db 117 RIMEKADSNKTRIDEANQ 134
|||||

RESULT 3
O93579 O93579 PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein
DE 25.2).
GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage."
RL J. Neurosci. Res. 0:0-0(1998).
DR EMBL; AF091594; AAC64290.1; -.
DR EMBL; AF091596; AAC73007.1; -.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.

DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match 89.9%; Score 80; DB 13; Length 206;
Best Local Similarity 88.9%; Pred. No. 7.3e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||||
Db 180 RIMEKADSNKTRIDEANQ 197
|||||

RESULT 5
Q8AXM1 Q8AXM1 PRELIMINARY; PRT; 206 AA.
AC Q8AXM1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNAP25b (Hypothetical protein).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
```


RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335587; AA013789.1; -.
DR EMBL; BC055981; AAH55981.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Hypothetical protein.
SQ SEQUENCE 206 AA; 23187 MW; 7D3B2071E577F02 CRC64;

Query Match 89.9%; Score 80; DB 13; Length 206;
Best Local Similarity 88.9%; Pred. No. 7.3e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||:|||||
Db 180 RIMEKADSNKTRIDEANQ 197

RESULT 6
Q8JIS7 ID Q8JIS7 PRELIMINARY; PRT; 204 AA.
AC Q8JIS7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNAP-23.
GN XOSNAP-23.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Mashima J., Nagahama M., Hattuzawa K., Tani K., Kikuchi F.,
RA Horigome T., Yamamoto A., Tagaya M.;
RT "Evidence for the involvement of alpha-SNAP and SNAP-23 in the fusion
of nuclear membrane vesicles.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033718; BAC06591.1; -.

DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNAP-25; 2.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 204 AA; 22771 MW; D034F75E638E8805 CRC64;

Query Match 78.7%; Score 70; DB 13; Length 204;
Best Local Similarity 82.4%; Pred. No. 0.0029;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
|||:|||||
Db 180 RINEKAETNKTRIDEAN 196

RESULT 7
Q7ZVE4 ID Q7ZVE4 PRELIMINARY; PRT; 214 AA.
AC Q7ZVE4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to synaptosomal-associated protein, 23 kDa.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045896; AAH45896.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 214 AA; 23670 MW; 5B43808BA6645A4C CRC64;

Query Match 78.7%; Score 70; DB 13; Length 214;
Best Local Similarity 77.8%; Pred. No. 0.003;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
|||:|||||
Db 191 RITDKADMKNKTRIDEANQ 208

RESULT 8
Q8T3S4 ID Q8T3S4 PRELIMINARY; PRT; 212 AA.
AC Q8T3S4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNAP25 fusion protein.
OS Loligo pealeii (Longfin squid).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Lolliginidae; Loligo.
OX NCBI_TaxID=6621;
RN [1]
RP SEQUENCE FROM N.A.
RA Bracher A., Kadlec J., Betz H., Weissenhorn W.;
RT "X-ray structure of a neuronal complexin/SNARE complex from squid.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Dresbach T., O'Connor V., Burns M., Augustine G., Betz H.;
RT "Squid SNAP25.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY092757; AAM18191.1; -.
DR PDB; 1L4A; 31-JUL-02.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS50192; T SNARE; 2.
SQ SEQUENCE 212 AA; 23816 MW; 127601619DE79E2D CRC64;

Query Match 73.0%; Score 65; DB 5; Length 212;
Best Local Similarity 66.7%; Pred. No. 0.019;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
||:||||:||||:
Db 187 RIQKKAESNESRIDEANK 204

RESULT 9
O35620 PRELIMINARY; PRT; 210 AA.
AC O35620;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE 23kDa synaptosomal associated protein.
GN SNAP23 OR MSNAP-23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Olken S.K., Doerre S., Corley R.B.;
RT "SNARE expression in mouse plasma cells";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF007169; AAB62932.1; -.
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS50192; T SNARE; 2.
SQ SEQUENCE 210 AA; 23277 MW; FB752FB58D5AE6D9 CRC64;

Query Match 66.3%; Score 59; DB 11; Length 210;
Best Local Similarity 70.6%; Pred. No. 0.17;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
:||||:||||:
Db 185 KITEKADTNKNRIDIAN 201

RESULT 10
O70377 PRELIMINARY; PRT; 210 AA.
AC O70377;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SNAP-23.
GN SNAP-23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162237; PubMed=10051443;

RA St-Denis J.F., Cabaniols J.P., Cushman S.W., Roche P.A.;
RT "SNAP-23 participates in SNARE complex assembly in rat adipose cells";
RL Biochem. J. 338:709-715(1999).
DR EMBL; AF052596; AAC06031.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS50192; T SNARE; 2.
SQ SEQUENCE 210 AA; 23235 MW; OD63E3A6F9FE3BA2 CRC64;

Query Match 66.3%; Score 59; DB 11; Length 210;
Best Local Similarity 70.6%; Pred. No. 0.17;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
:||||:||||:
Db 185 KITEKADTNKNRIDIAN 201

RESULT 11
O09044 PRELIMINARY; PRT; 210 AA.
AC O09044;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SYNDET (SNAP-23) (Synaptosomal-associated protein, 23kD).
GN SNAP23 OR SNPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat;
RX MEDLINE=97312558; PubMed=9168999;
RA Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H.,
RA Niki T., Okazawa H., Kubota T., Kasuga M.;
RT "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c";
RL Biochem. Biophys. Res. Commun. 234:257-262(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97220227; PubMed=9067602;
RA Wang G., Witkin J.W., Hao G., Bankaitis V.A., Scherer P.E.,
RA Baldini G.;
RT "Syndet is a novel SNAP-25 related protein expressed in many tissues";
RL J. Cell Sci. 110:505-513(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Vaidyanathan V.V., Roche P.A.;
RT "Structure and chromosomal localization of the mouse SNAP-23 gene";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AB000822; BAA20345.1; -.
DR EMBL; U73143; AAB53597.1; -.
DR EMBL; AF213257; AAF23503.1; -.
DR EMBL; AF213251; AAF23503.1; JOINED.
DR EMBL; AF213252; AAF23503.1; JOINED.
DR EMBL; AF213253; AAF23503.1; JOINED.
DR EMBL; AF213254; AAF23503.1; JOINED.
DR EMBL; AF213255; AAF23503.1; JOINED.
DR EMBL; AF213256; AAF23503.1; JOINED.
DR EMBL; AK019162; BAB31577.1; -.
DR PIR; JC5512; JC5512.
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 210 AA; 23261 MW; 6919E127E16BA2C9 CRC64;

Query Match 66.3%; Score 59; DB 11; Length 210;
Best Local Similarity 70.6%; Pred. No. 0.17;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
:|:|:|:|:|:|:|:|:|
Db 185 KITEKADTNKNRIDIAN 201

RESULT 12
Q9D3L3 PRELIMINARY; PRT; 221 AA.
AC Q9D3L3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosomal-associated protein, 23kD.
GN SNAP23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
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RL Nature 409:685-690(2001).
DR EMBL; AK017311; BAB30686.1; -.
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 221 AA; 24550 MW; 368862BE7232DEFB CRC64;

Query Match 66.3%; Score 59; DB 11; Length 221;
Best Local Similarity 70.6%; Pred. No. 0.18;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
:|:|:|:|:|:|:|:|:|
Db 196 KITEKADTNKNRIDIAN 212

RESULT 13
O96578 PRELIMINARY; PRT; 90 AA.
AC O96578;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-5 (Fragment).
GN SNAP-5.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence
variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
DR EMBL; AF091602; AAC69878.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
FT NON TER 1
SQ SEQUENCE 90 AA; 10136 MW; E502DB954676E9F7 CRC64;

Query Match 56.2%; Score 50; DB 5; Length 90;
Best Local Similarity 61.1%; Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
||:|:|:|:|:|:|
Db 66 RIKNKAESNEERIKVANQ 83

RESULT 14
O96576 PRELIMINARY; PRT; 125 AA.
AC O96576;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-3 (Fragment).
GN SNAP-3.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
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Job time : 36.5135 secs

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OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence
RT variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
DR EMBL; AF091600; AAC69876.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
FT NON TER 1
SQ SEQUENCE 125 AA; 13985 MW; 72B032879858C316 CRC64;

Query Match 56.2%; Score 50; DB 5; Length 125;
Best Local Similarity 61.1%; Pred. No. 2.9;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
Db 100 RIKKKAESNEERIKVANQ 117

RESULT 15
O62414
ID O62414 PRELIMINARY; PRT; 207 AA.
AC O62414;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Y22F5A.3.
GN Y22F5A.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL021479; CAA16322.2; -.
DR PIR; T26553; T26553.
DR WormPep; Y22F5A.3; CE32008.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
KW Hypothetical protein.
SQ SEQUENCE 207 AA; 23092 MW; 547031DF8C8C5C22 CRC64;

Query Match 56.2%; Score 50; DB 5; Length 207;
Best Local Similarity 50.0%; Pred. No. 4.8;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
Db 182 RIHDKAQSNVVRVESANK 199

Search completed: March 9, 2004, 11:09:35
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 22.4211 Seconds
(without alignments)
84.434 Million cell updates/sec

Title: US-10-030-485A-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	100.0	18	6 Q9TRF1	Q9trf1 bos taurus
2	30	100.0	82	5 Q8MZ33	Q8mz33 drosophila
3	30	100.0	82	5 Q81QC6	Q8iqc6 drosophila
4	30	100.0	107	4 Q8N3E7	Q8n3e7 homo sapien
5	30	100.0	149	16 Q92XY8	Q92xy8 rhizobium m
6	30	100.0	206	13 Q8AXM2	Q8axm2 xenopus lae
7	30	100.0	206	13 Q8AXM1	Q8axm1 xenopus lae
8	30	100.0	216	4 Q7Z390	Q7z390 homo sapien
9	30	100.0	297	4 Q8N417	Q8n417 homo sapien
10	30	100.0	507	4 Q86VG8	Q86vg8 homo sapien
11	30	100.0	537	5 Q9W2P0	Q9w2p0 drosophila
12	30	100.0	760	10 Q7XR85	Q7xr85 oryza sativ
13	30	100.0	904	4 Q81WC1	Q81wcl homo sapien
14	27	90.0	21	15 Q87583	Q87583 chimpanzee
15	27	90.0	81	16 Q7V6N4	Q7v6n4 prochloroco
16	27	90.0	87	11 Q8BT51	Q8bt51 mus musculu

17	27	90.0	96	4 Q9NYJ1	Q9nyj1 homo sapien
18	27	90.0	105	4 Q96G37	Q96g37 homo sapien
19	27	90.0	112	16 Q54113	Q54113 streptomyce
20	27	90.0	117	16 Q9A4P3	Q9a4p3 caulobacter
21	27	90.0	122	4 Q9BTB7	Q9btb7 homo sapien
22	27	90.0	128	16 Q8PFC6	Q8pfc6 xanthomonas
23	27	90.0	130	15 Q76943	Q76943 human immun
24	27	90.0	135	16 Q8P3U7	Q8p3u7 xanthomonas
25	27	90.0	148	10 Q84MC4	Q84mc4 arabidopsis
26	27	90.0	162	16 Q66898	Q66898 aquifex aeo
27	27	90.0	165	10 Q9XHP7	Q9xhp7 ceratopteri
28	27	90.0	209	16 Q88Q68	Q88q68 pseudomonas
29	27	90.0	210	2 Q9RPW1	Q9rpw1 bacillus me
30	27	90.0	210	10 Q9SE48	Q9se48 oryza sativ
31	27	90.0	210	10 Q9SE47	Q9se47 oryza sativ
32	27	90.0	210	10 Q7XI40	Q7xi40 oryza sativ
33	27	90.0	222	5 Q8SXX3	Q8sxx3 drosophila
34	27	90.0	238	4 Q86TV0	Q86tv0 homo sapien
35	27	90.0	252	16 Q99YW2	Q99yw2 streptococc
36	27	90.0	252	16 Q8K6S1	Q8k6s1 streptococc
37	27	90.0	256	16 Q8E6N2	Q8e6n2 streptococc
38	27	90.0	256	16 Q8E178	Q8e178 streptococc
39	27	90.0	257	16 Q9HU49	Q9hu49 pseudomonas
40	27	90.0	257	16 Q8PMK9	Q8pmk9 xanthomonas
41	27	90.0	258	16 Q8PAV7	Q8pav7 xanthomonas
42	27	90.0	264	16 Q9RS89	Q9rs89 deinococcus
43	27	90.0	275	10 Q8H688	Q8h688 oryza sativ
44	27	90.0	283	10 Q43508	Q43508 lycopersico
45	27	90.0	284	16 Q98GM6	Q98gm6 rhizobium l

ALIGNMENTS

RESULT 1

Q9TRF1	ID	Q9TRF1	PRELIMINARY;	PRT;	18 AA.
AC	Q9TRF1;				
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)			
DE	Soluble N-ethylmaleimide-sensitive attachment protein SNAP-25				
DE	(Fragment).				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=93374072; PubMed=8365494;				
RA	Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tsugita A., Odani S.,				
RA	Abe T.;				
RL	FEBS Lett. 330:236-240(1993).				
SQ	SEQUENCE 18 AA; 2120 MW; 371FC93766C4A7BB CRC64;				

Query Match 100.0%; Score 30; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
| | | | |
Db 2 EEMQRR 7

RESULT 2

Q8MZ33	ID	Q8MZ33	PRELIMINARY;	PRT;	82 AA.
AC	Q8MZ33;				
DT	01-OCT-2002	(TREMBLrel. 22, Created)			
DT	01-OCT-2002	(TREMBLrel. 22, Last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			
DE	RE03722p.				

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GN BCNNA:RE03722.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY113381; AAM29386.1; -.
DR FlyBase; FBgn0063077; BCDNA:RE03722.
SQ SEQUENCE 82 AA; 9539 MW; E0F4D3104060796E CRC64;

Query Match 100.0%; Score 30; DB 5; Length 82;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 58 EEMQRR 63

RESULT 3
Q81QC6 PRELIMINARY; PRT; 82 AA.
AC Q81QC6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG32039-PA.
GN CG32039.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter G., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003552; AAN1959.1; -.
DR FlyBase; FBgn0052039; CG32039.
SQ SEQUENCE 82 AA; 9540 MW; E0FE73104AC0796E CRC64;

Query Match 100.0%; Score 30; DB 5; Length 82;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 58 EEMQRR 63

RESULT 4
Q8N3E7 PRELIMINARY; PRT; 107 AA.
AC Q8N3E7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP76111323.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amygdala;
RA Bloeker H., Bocher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834393; CAD39055.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 107 AA; 13460 MW; A411E3F036789795 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 94 EEMQRR 99

RESULT 5
Q92XY8
ID Q92XY8 PRELIMINARY; PRT; 149 AA.
AC Q92XY8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein RA1100.
GN RA1100 OR SMA2009.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSMA (megaplasmid 1).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSMA megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR EMBL; AE007296; AAK65758.1; -.
DR PIR; D95399; D95399.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR004360; Gly_bleo_diox.
DR Pfam; PF00903; Glyoxalase; 1.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 149 AA; 16237 MW; 86C045BFD8F5ACF5 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 149;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 137 EEMQRR 142

RESULT 6
Q8AXM2
ID Q8AXM2 PRELIMINARY; PRT; 206 AA.
AC Q8AXM2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNAP25a.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

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OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335586; AAO13788.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match 100.0%; Score 30; DB 13; Length 206;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 7
Q8AXM1
ID Q8AXM1 PRELIMINARY; PRT; 206 AA.
AC Q8AXM1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNAP25b (Hypothetical protein).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335587; AA013789.1; -.
DR EMBL; BC055981; AAH55981.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS0192; T-SNARE; 2.
KW Hypothetical protein.
SQ SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;

Query Match 100.0%; Score 30; DB 13; Length 206;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 8
Q7Z390
ID Q7Z390 PRELIMINARY; PRT; 216 AA.
AC Q7Z390;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686C04150 (Fragment).
GN DKFZP686C04150.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human colon endothel primary cell culture;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538046; CAD97985.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 216 AA; 24473 MW; 68CB647EB074786B CRC64;

Query Match 100.0%; Score 30; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 203 EEMQRR 208

RESULT 9
Q8N417
ID Q8N417 PRELIMINARY; PRT; 297 AA.
AC Q8N417;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036844; AAH36844.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 297 AA; 32380 MW; 2AAB420A29422FEF CRC64;

Query Match 100.0%; Score 30; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 284 EEMQRR 289

RESULT 10
Q86VG8
ID Q86VG8 PRELIMINARY; PRT; 507 AA.
AC Q86VG8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim N.-S., Shon H.-Y., Oh J.-H., Lee J.-Y., Kim J.-M., Hahn Y.,
RA Park H.-S., Kim S., Kim Y.S.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452716; AAP13351.1; -.
KW Hypothetical protein.
SQ SEQUENCE 507 AA; 54948 MW; EEA3E083E79CAD26 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
Db 494 EEMQRR 499

RESULT 11
Q9W2P0
ID Q9W2P0 PRELIMINARY; PRT; 537 AA.
AC Q9W2P0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CG3221 protein (LD38682P).
GN CG3221.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Blazewicz R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazewicz R.G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003452; AAF46650.1; -.
DR EMBL; AY058678; AAL13907.1; -.
DR FlyBase; FBgn0034569; CG3221.
SQ SEQUENCE 537 AA; 62576 MW; 94FBA570315F6FDF CRC64;

Query Match 100.0%; Score 30; DB 5; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 27 EEMQRR 32

RESULT 12

Q7XR85
ID Q7XR85 PRELIMINARY; PRT; 760 AA.

AC Q7XR85;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNBa0011L07.16 protein.
GN OSJNBa0011L07.16.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartodeae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.

RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,

RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606587; CAE02792.1; -.
SQ SEQUENCE 760 AA; 82554 MW; 80C7507DACBB8643 CRC64;

Query Match 100.0%; Score 30; DB 10; Length 760;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 320 EEMQRR 325

RESULT 13

Q8IWC1
ID Q8IWC1 PRELIMINARY; PRT; 904 AA.

AC Q8IWC1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC040518; AAH40518.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR008604; E-MAP-115.
DR Pfam; PF05672; E-MAP-115; 1.
DR PROSITE; PS00402; BPD_TRANS_PNN_MEMBER; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 904 AA; 101665 MW; 6C527C706D3EB11B CRC64;

Query Match 100.0%; Score 30; DB 4; Length 904;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 652 EEMQRR 657

RESULT 14

Q87583
ID Q87583 PRELIMINARY; PRT; 21 AA.

AC Q87583;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Rev protein (Fragment).
GN REV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=P051;
RX MEDLINE=97138325; PubMed=8985351;
RA Bibollet-Ruche F., Brengues C., Galat-Luong A., Galat G., Pourrut X.,

RA Vidal N., Veas F., Durand J.P., Cuny G.;
RT "Genetic diversity of simian immunodeficiency viruses from west
RT African green monkeys: evidence of multiple genotypes within
RT populations from the same geographical locale.";
RL J. Virol. 71:307-313(1997).
DR EMBL; U37201; AAC56137.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON TER 21 21
SQ SEQUENCE 21 AA; 2599 MW; 6AD581D9CFE92914 CRC64;

Query Match 90.0%; Score 27; DB 15; Length 21;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
||:||||
Db 6 EELQRR 11

RESULT 15
Q7V6N4
ID Q7V6N4 PRELIMINARY; PRT; 81 AA.
AC Q7V6N4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved hypothetical.
GN PM11118.
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation."
RL Nature 424:1042-1047(2003).
DR EMBL; BX572098; CAE21293.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 81 AA; 9436 MW; BE9BD0715D4E40E8 CRC64;

Query Match 90.0%; Score 27; DB 16; Length 81;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
||:||||
Db 62 EELQRR 67

Search completed: March 4, 2004, 08:29:14
Job time : 24.4211 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 8.21053 Seconds
(without alignments)
70.294 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	56	2 S36812	probable synapse-a
2	30	100.0	149	2 D95399	protein [imported]
3	30	100.0	206	2 A37861	synaptosomal-assoc
4	30	100.0	206	2 I53735	nerve terminal pro
5	30	100.0	206	2 I67823	nerve terminal pro
6	30	100.0	206	2 A33623	synaptosomal-assoc
7	30	100.0	249	2 S38308	SNAP-25 protein -
8	30	100.0	249	2 S38309	SNAP-25 protein -
9	27	90.0	112	2 T34589	hypothetical prote
10	27	90.0	117	2 C87594	hypothetical prote
11	27	90.0	162	1 F70358	hydrogenase matura
12	27	90.0	257	2 C83005	conserved hypothet
13	27	90.0	264	2 D75298	carbonic anhydrase
14	27	90.0	283	2 S42393	G-box-binding prot
15	27	90.0	303	2 S58243	pyrroloquinoline q
16	27	90.0	309	2 E69200	conserved hypothet
17	27	90.0	319	2 C83892	proline dehydrogen
18	27	90.0	327	2 T06602	hypothetical prote
19	27	90.0	333	2 T05121	hypothetical prote
20	27	90.0	378	2 JC5658	LIM domain-contain
21	27	90.0	407	2 C97212	HD gyp hydrolase d
22	27	90.0	450	2 C75033	adenylosuccinate l
23	27	90.0	450	2 H71135	probable adenylosu
24	27	90.0	453	2 S52690	hypothetical prote
25	27	90.0	472	2 AB3239	conserved hypothet
26	27	90.0	509	2 A71254	probable glu-trna
27	27	90.0	528	2 B75310	conserved hypothet
28	27	90.0	534	2 T39903	serine-rich protei
29	27	90.0	622	2 S51972	SPC72 protein - ye

30	27	90.0	647	2 C71534	probable transglyc
31	27	90.0	689	2 S17875	polynucleotide ade
32	27	90.0	702	2 C69999	DNA translocase st
33	27	90.0	727	2 S54512	hypothetical prote
34	27	90.0	739	2 S18642	polynucleotide ade
35	27	90.0	740	2 S17925	polynucleotide ade
36	27	90.0	783	2 AF1275	DNA translocase ho
37	27	90.0	784	2 AF1638	DNA translocase ho
38	27	90.0	809	1 QQBE34	BBLF4 protein - hu
39	27	90.0	856	2 T13159	E1B-55kDa-associa
40	27	90.0	869	2 A25945	coagulation factor
41	27	90.0	947	2 B86231	hypothetical prote
42	27	90.0	961	2 A55380	faciogenital dyspl
43	27	90.0	1203	2 T21275	hypothetical prote
44	27	90.0	1274	2 A89959	hypothetical prote
45	27	90.0	1328	2 AE2351	protoporphyrin IX

ALIGNMENTS

RESULT 1

S36812

probable synapse-associated 28K protein - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C;Accession: S36812
R;Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A;Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A;Reference number: S36811; MUID:93374072; PMID:8365494
A;Accession: S36812
A;Molecule type: protein
A;Residues: 1-56 <HOR>
A;Experimental source: brain

Query Match 100.0%; Score 30; DB 2; Length 56;
Best Local Similarity 100.0%; Pred.No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

Db 2 EEMQRR 7

RESULT 2

D95399
protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSyma
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95399
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9886, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: D95399
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65758.1; PID:gl4524256; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSyma
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma2009

RESULT 8

S38309
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38309
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38309
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 30; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
Db 12 EEMQRR 17

RESULT 9

T34589
hypothetical protein SC10A5.22 SC10A5.22 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34589
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z21548
A:Accession: T34589
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-112 <MUR>
A:Cross-references: EMBL:AL021529; PIDN:CAA16454.1; GSPDB:GN00070; SCOEDB:SC10A5.22
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC10A5.22

Query Match 90.0%; Score 27; DB 2; Length 112;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
Db 97 EELQRR 102

RESULT 10

C87594
hypothetical protein CC2787 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: C87594
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87594
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <STO>
A:Cross-references: GB:AE005673; NID:gl3424387; PIDN:AAK24751.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2787

Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
Db 74 DEMQRR 79

RESULT 11

F70358
hydrogenase maturation factor hupD [similarity] - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2003
C:Accession: F70358
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.

Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70358
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <AQF>

A:Cross-references: GB:AE000701; GB:AE000657; NID:g2983260; PIDN:AAC06858.1; PID:g29832
A:Experimental source: strain VF5
C:Genetics:
A:Gene: hupD
C:Superfamily: [NiFe]-hydrogenase maturation protease

Query Match 90.0%; Score 27; DB 1; Length 162;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
Db 23 EELQRR 28

RESULT 12

C83005
conserved hypothetical protein PA5135 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83005
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83005
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <STO>
A:Cross-references: GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AAG08520.1; GSPDB:GN00
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA5135

Query Match 90.0%; Score 27; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
Db 143 EELQRR 148

RESULT 13

D75298
carbonic anhydrase - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C;Accession: D75298
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: D75298
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-264 <WHI>
 A;Cross-references: GB:AE002056; GB:AE000513; NID:g6460037; PIDN:AAF11784.1; PID:g646004
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR2238
 A;Map position: 1
 C;Superfamily: Escherichia coli carbonate dehydratase

Query Match 90.0%; Score 27; DB 2; Length 264;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 ||:||||
 Db 34 EELQRR 39

RESULT 14
 S42393
 G-box-binding protein - tomato
 C;Species: Lycopersicon esculentum (tomato)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Sep-2000
 C;Accession: S42393
 R;Meier, I.; Gruissem, W.
 Nucleic Acids Res. 22, 470-478, 1994
 A;Title: Novel conserved sequence motifs in plant G-box binding proteins and implication
 A;Reference number: S42392; MUID:94173701; PMID:8127687
 A;Accession: S42393
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-283 <MEI>
 A;Cross-references: EMBL:X74942; NID:g456752; PIDN:CAA52896.1; PID:g456753
 C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
 F;182-222/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 90.0%; Score 27; DB 2; Length 283;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 ||:||||
 Db 213 EELQRR 218

RESULT 15
 S58243
 pyroloquinoline quinone synthesis B - Pseudomonas fluorescens
 C;Species: Pseudomonas fluorescens
 C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
 C;Accession: S58243
 R;Schnider, U.; Keel, C.; Defago, G.; Haas, D.
 submitted to the EMBL Data Library, May 1995
 A;Description: Tn5-directed cloning of pqg genes from Pseudomonas fluorescens CHA0: thei
 A;Reference number: S58239
 A;Accession: S58243
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-303 <SCH>
 A;Cross-references: EMBL:X87299; NID:g929799; PIDN:CAA60733.1; PID:g929805

Query Match 90.0%; Score 27; DB 2; Length 303;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 ||:||||
 Db 227 DEMQRR 232

Search completed: March 4, 2004, 08:29:53
 Job time : 10.2105 secs